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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic August 10, 2004, 17:10:22; Search time 10.9751 Seconds (without alignments) 7635.278 Million cell updates/sec Run on:

US-10-001-857-41 Title: Perfect score:

1 cogccogggcaggtacctaa......gcaaattcctcaagaatatg 151 Sequence:

Scoring table:

682709 segs, 277475446 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents NA:*
1: /cgT2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgT2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgT2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgT2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgT2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgT2_6/prodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 840, App	Sequence 1, Appli	42,	42,	1, 1	14,	ı,	Ļ	4	Sequence 17, Appl	1, 1	3, 7	48	1,	Sequence 87, Appl	666	1,	204	303	'n	δ,	Sequence 11, Appl	H	909	H	1,	13,
	ai.	US-09-489-039A-840	US-08-952-674-1	US-08-480-173A-42	US-08-484-408A-42	US-08-890-735C-1	US-10-104-966-14	US-08-799-569-1	US-09-570-546-1	US-09-146-072A-1	US-09-128-155-17	US-09-719-528A-1	US-09-751-389-3	US-09-671-317-485	US-08-916-421B-1	US-08-976-259-87	US-09-328-352-999	US-09-426-290-1	US-09-621-976-2040	US-09-620-312D-303	US-09-514-907A-5	US-09-896-994-5	US-10-027-983-11	US-08-545-528D-1	US-09-328-111-606	US-09-545-686-1	US-10-096-571-11	US-10-096-571-13
	DB	4	4	M	m	4	4	ო	4	4,	e	4	4	4	4	4	4	4	4	4	4	4	4	4	m	4	4	4
	Length	1689	4421	2348	2348	3182	3182	5618	5618	5618	176373	3215	786431	49312	1664976	595	1740	168575	501	2089	3069	3069	392000	580073	577	1671	2111	2111
* Query	Match	20.5	20.0	19.5	19.5	19.5	19.5	19.5	19.5	19.5	19.2	18.9	18.5	18.4	18.1	18.0	17.7	17.7	17.6		17.6	17.6	17.6			17.5	17.4	17.4
	Score	31		29.4	29.4	29.4	29.4	29.4	29.4	29.4	29	28.6	28	27.8	27.4	27.2	26.8	26.8	26.6	26.6	26.6	26.6	26.6	26.6	26.4	26.4	26.2	26.2
Result	No.	ט	c 5	3	C 4	C 2	و ت	c 2	ω ω	6 2	c 10	c 11	12	13	c 14	15	16	c 17	c 18	c 19	20	21	22	c 23	c 24	25	c 26	c 27

Sequence 1, Appli Sequence 1, Appli	73,	Sequence 1019, Ap Sequence 592, App	Sequence 3, Appli Sequence 11, Appl	٦,	Sequence 1, Appli	Sequence 1035, Ap	Seguence 8, Appli	Sequence 5, Appli	Sequence 1, Appli				
US-08-452-075-1 US-09-231-061-1	US-09-313-294A-7377	US-08-956-171E-1019 US-08-956-171E-592	US-09-470-512A-3	4 US-09-557-884-1	4 US-09-643-990A-1	US-09-489-039A-1035	US-09-306-446C-8	US-08-463-092B-5	US-08-462-109A-5	US-08-460-907B-5	US-08-463-179A-5	US-08-461-384B-5	US-08-545-528D-1
2841 2 2841 3	312 4	779 4 1449 4	41708 4	830121 4	830121 4	618 4	5108 4	5889 1	5889 2	5889 2	5889 3	5889 3	580073 4
17.4	17.2	17.2	17.2 4	17.2 18	17.2 18	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1 58
26.2	79.7 70.7	26 26	26 26	7 2 2	26	25.8	25.8	25.8	25.8	25.8	25.8	25.8	25.8
c 28	0 3 31	ი 33 33	3. 3. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.	36.0	c 37	c 38	39	٥ 40	c 41	c 42	c 43	C 44	45

ALIGNMENTS

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APPLICANT: Gary Breton US/09489039A

Sequence 840, Application US/09489039A

Sequence 840, Application US/09489039A

Sequence 840, Application US/09489039A

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLES: 2709.2004001
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PAPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

LINGTH: 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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US-08-952-674-1/c
108-952-674-1/c
; Sequence 1, Application US/08952674
; Parent No. 6623951
; GERERAL INFORMATION:
; APPLICANT: Hoberbreiger, Peter
; APPLICANT: Hoberbreiger, Peter
; APPLICANT: Ludwig, Weiss
; TITLE OF INVENTION: HBV Vectors and Cells for Producing Same
; FILE REFERENCE: HBV Vectors
; CURRENT APPLICATION NUMBER: US/08/952,674
; CURRENT APPLICATION NUMBER: US/08/952,674
; RARLIER PILING DATE: 1996-03-02
; RARLIER FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.5%; Score 31; DB 4; Length 1689; 68.3%; Pred. No. 0.24; tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CRGANISM: Klebsiella pneumoniae
US-09-489-039A-840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 68.3 Matches 43; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                         18 TARACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTAAAGCGCCGC
                                                                                                                                                                                                                                                                                                                                             4117 CCCCAACTCCTCCAGTCCTTAAACAAACAGTCTTTGAAGTATGCCTCAAGGTCG 4063
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                        78 ATCAACCTICICIGCCTAITAAAATAAAATGICATAAAACTCCTGCAAGGIGG 132
                                                                                                                                                                                   .
0
                                                  FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pHBV/VI
US-08-952-674-1
                                                                                                                                        Score 30.2; DB 4; Length 4421;
Pred. No. 0.71;
0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42, Application US/08480173A
Patent No. 6072049
GENERAL INFORMATION:
APPLICANT: Thoma, Hans A
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Popovich & Wiles, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,173A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "S1 start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "S2 start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: POPOVICh, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELECOWMUNICATION INFORMATION:
TELECHONE: 612-334-8991
TELECHONE: 612-334-8994
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 2348 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Popovich & Wiles, P.A. STREET: 80 S. 8th Street, Suite 1902 CITX: Minneapolis
                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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LOCATION: 12...14
OTHER INFORMATION: /note=
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                                                                                                                                   Query Match 20.0%;
Best Local Similarity 53.9%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 336..338
OTHER INFORMATION: /not
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OTHER INFORMATION:
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US-08-480-173A-42/c
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DB 3; Length 2348;

Score 29.4;

19.5%;

Query Match

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                                                                                             2154 cagaccaaritarigccracagccrccragiacaaagaccriraaccraarcrccccc 2095
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                                                       22 CAGGCCAAATGTTGCCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAAGCGCCGCATCA
                      0; Gaps
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                                                                                                                                                                         2094 AACTCCTCCRGTCTTTAAACAACAGTCTTTGAAGTATGCCTCAAGGTCG 2044
                                                                                                                                    82 ACCTICICICCCTATTAAAATAAAATGICATAAACTCATCCTGCAAGGIGG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POPOVICH, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MEDIO3USD4
TELEPHONE: 612-334-8994
TELEPHONE: 612-334-8994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "S1 start codon"
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i LCCATION: 508..510
corner INFORMATION: /note= "S start codon"
US-08-484-4088-42
54.1%; Pred. No. 1;
tive 0; Mismatches
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LOCATION: 12...14
OTHER INFORMATION: /note=
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LOCATION: 336..338
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2348 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                    60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 612-334-8994
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 60; Conserv
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APPLICANT: Michel, Marie-Louise
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Best Local Similarity
Matches 60; Conserv
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                                             US-08-799-569-1/c
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                            RESULT 7
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2094 AACTCCTCCCAGTCTTTAAACAACAGTCTTTGAAGTATGCCTCAAGGTCG 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1743 AACTCCTCCCAGTCTTTAAACAAACAGTCTTTGAAGTATGCCTCAAGGTCG 1693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29.4; DB 4; Length 3182; Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Matti Sallberg
APPLICANT: Catharina Hulleren
TITLE OF INVENTION: WETHODS OF USE THEREOF
TITLE OF INVENTION: WETHODS OF USE THEREOF
TITLE OF INVENTION: WETHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: 09/705,547
PRIOR PRILING DATE: 2002-03-22
PRIOR PRILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Hepatitis B virus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.2;
0; Mismatches
                                                                                                                                                                                       APPLICANT: Bristol. Myers Squibb Company TITLE OF INVENTION: HEPADNAVIRUS CORES FILE REFERRNCE: DC44A CURRENT APPLICATION NUMBER: US/08/890,735C CURRENT APPLICATION NUMBER: 18707-11 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/10104966 Patent No. 6680059
                                                                                                       RESULT 5
US-08-890-735C-1/c
; Sequence 1, Application US/08890735C
; Parent No. 6518014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.5%;
54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Hepatitis B Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60; Conservative
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-10-104-966-14/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 14
LENGTH: 3182
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                                                                                                                                                                                                                                                                                                                                                                                                         3182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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Matches
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Sequence 1, Application US/08799569
Patent No. 6133244
GENERAL INPORMATION:
APPLICANT: Marchel, Maryline
APPLICANT: Mancine, Maryline
TITLE OF INVENTION: Oucleotide Vector, Composition
TITLE OF INVENTION: Concaining Such Vector, and Vaccine for Immunization
TITLE OF INVENTION: Against Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGCCAAATGTTGCCTTTGGGGGTTCCTGTTTCAACAGCATGGTGTGAAGCGCCGCATCA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2525 Aachecheceagieithaaacaanchirtaaagrahageereaagice 2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 ACCTICICICCCTATIAAAAIAAAAIGICAIAAACICCAICCIGCAAGGIGG 132
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                                                                                                                                                                                                                                                        Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/799,569
FILING DATE: 12-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
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Pred. No. 1.5;
0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0128-01000
TELECOMMUNICATION INFORMATION:
TELEPRINE: (202) 408-400
ITELEPRINE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/706,337
FILING DATE: 30-AUG-1996
PRIOR APPLICATION NUMBER: US 08/633,821
APPLICATION NUMBER: US 08/633,821
FILING DATE: 22-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/00483
FILING DATE: 27-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09570546; Patent No. 6429201; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) US-08-799-569-1
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54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meyers, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY di
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan,
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Gaps

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2585 CAGACCAÁTTTATGCCTACCTCCTAGTACAÁAGACCTTTAACCTAÁTCTCCTCCCC 2526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cccrcrcaaracraraagrercraaarrirgacaraggerracraraggers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 CAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAAGCGCCGCATCA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CCCGGGCAGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTTCCTGTTTCAACAGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 ACCTICICIGCCTATIAAAATAAAATGTCATAAACTCATCCTGCAAGGTGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAAAACAGAATAATCTTTGCTTTTTCAATCTTAAATTTAAATGTTAGA 8287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
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19.5%; Score 29.4; DB 4;
Best Local Similarity 54.1%; Pred. No. 1.5;
Matches 60; Conservative 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                 PRIOR APPLICATION NUMBER: US 08/633,821
PRIOR FILING DATE: 1996-08-02
PRIOR PLING DATE: 1996-08-02
PRIOR PRIOR PLING DATE: 1994-04-27
PRIOR PRIUNG DATE: 1993-10-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: PATENTIN VERSION 3.2
LENGTH: 5618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                           FEATURE:
COTHER INFORMATION: Synthetic Sequence
US-09-146-072A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09128155
Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-719-528A-1/c
; Sequence 1, Application US/09719528A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i LOCATION: (1)...(176373)
i OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 53.6%;
59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 59; Conserv
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Sequence 1, Application US/09146072A

Patent No. 6635624

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Whalen, Robert G.

APPLICANT: Whalen, Robert G.

TITLE OF INVENTION: UNCLECTIOE VECTOR, COMPOSITION CONTAINING SUCH VECTOR AND VACCINE

TITLE OF INVENTION: FOR IMMUNIZATION AGAINST HERATITIS

FILE REFERENCE: C01040.70004.US

CURRENT APPLICATION NUMBER: US/09/146,072A
Mancine, Maryline
TITLE OF INVENTION: Nucleotide Vector, Composition
Containing Such Vector, and Vaccine for Immunization
Against Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2585 CAGACCAATITATGCCTACAGCCTCCTAGTACAAAGACCTTTAACCTAATCTCCTCCCC 2526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5618;
                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,546
FILING DATE: 12-May-2000
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET VUMBER: 03495.0128-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/799,569
FILING DATE: «Uhrown»
APPLICATION NUMBER: US 08/706,337
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 08/633,821
FILING DATE: 22-APR-1996
APPLICATION NUMBER: RP 94/00483
FILING DATE: 27-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.5%; Score. 1.5, 54.1%; Pred. No. 1.5, ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-570-546-1
                                                                                                                                                                              STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                  Dunner
                                                                                              SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                           NUMBER OF
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
HIPPORT Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chan, Annick
FILE REFERENCE: 62.033.CIP
FILE REFERENCE: 62.033.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT FILING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US 09/536,178
FRIOR APPLICATION NUMBER: US 09/536,178
FRIOR APPLICATION NUMBER: DCT/IB00/00403
FRIOR APPLICATION NUMBER: US 60/126,269
FRIOR PILING DATE: 1999-03-25
FRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                          157775 GTTACTGTTACAGGAGCATATTCCTAAGTTAGTTTTCAATCTTGTCTGCCTATTAAGCTA 157834
                                                                                                                                                                                                                                                                                                     44 GITCCTGTTTCAACAGCATGGTGTGAAGCGCCGCATCAACCTTCTCTGCCTATTAAAATA
                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                Score 28; DB 4; Length 786431;
Pred. No. 45;
0; Mismatches 20; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : polymorphic base G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: 54667.7466
OTHER INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 485, Application US/09671317
Patent No. 6528260
                       FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(786431)

OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3
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                                                                                                                                                                                        Query Match 18.5%;
Best Local Similarity 66.7%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 7467..7725
OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 36905..36975
OTHER INFORMATION: exon 3
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NAME/KEY: misc feature
LOCATION: 45966..49312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: exon 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 7564
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LOCATION: 7649
ORGANISM: Human
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US-09-671-317-485
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Batent No. 663034

GRNREAL INFORMATION:
GRNREAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO1667

CURRENT APPLICATION NUMBER: US/09/751,389

CURRENT FILING DATE: 2001-01-02

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1805 TGAACAGACCAATTTATGCCTACAGCCTCCTAGTACATAAATCTTTAACCTAATCTCCTC 1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1745 CCCCAACTCCTCCCAGTCTTTAAACACACAGTCTTTGAAGTATGCCTCAAGGTCG 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                              TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 30-Apr-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 708-1800 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                 ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                          Chong Jin
Gek Keow
                                                                                                                  Zhao, Yi
Chen, Wei Ning
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 53.0
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                   STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              CITY: New York
  Patent No. 6558675
GENERAL INFORMATION:
APPLICANT: Oon,
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LENGTH: 786431
TYPE: DNA
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NAME/KEY, Prime, bind

LOCATION: 16730, 7648

OTHER INFORMATION: 10-286-375.mis complement

NAME/KEY: prime bind

LOCATION: 17239...17257

OTHER INFORMATION: 12-285-57.mis complement

NAME/KEY: prime bind

LOCATION: 17239...1727

OTHER INFORMATION: 12-425-57.mis complement

NAME/KEY: prime bind

LOCATION: 17239...1727

OTHER INFORMATION: 12-421-140.mis complement

NAME/KEY: prime bind

LOCATION: 17239...1627

OTHER INFORMATION: 12-421-140.mis complement

NAME/KEY: prime bind

LOCATION: 15230...16270

OTHER INFORMATION: 10-231-232.mis complement

NAME/KEY: prime bind

LOCATION: 165972...16590

OTHER INFORMATION: 10-239-201.mis complement

NAME/KEY: prime bind

LOCATION: 16572...16590

OTHER INFORMATION: 10-290-37.mis complement

NAME/KEY: prime bind

LOCATION: 16572...16590

OTHER INFORMATION: 10-290-37.mis complement

NAME/KEY: prime bind

LOCATION: 16572...16590

OTHER INFORMATION: 10-290-37.mis complement

NAME/KEY: prime bind

LOCATION: 16572...16590

OTHER INFORMATION: 10-290-37.mis complement

NAME/KEY: prime bind

LOCATION: 16572...16590

OTHER INFORMATION: 10-290-37.mis

NAME/KEY: prime bind

LOCATION: 16572...16590

OTHER INFORMATION: 10-290-37.mis complement

NAME/KEY: prime bind

LOCATION: 16572...16590

OTHER INFORMATION: 10-290-326.mis complement

NAME/KEY: prime bind

LOCATION: 16572...1650

OTHER INFORMATION: 10-280-326.mis complement

NAME/KEY: prime bind

LOCATION: 16572...1650

OTHER INFORMATION: 10-280-326.mis complement

NAME/KEY: prime binding

LOCATION: 16572...1650

OTHER INFORMATION: 10-280-326.probe

NAME/KEY: misc binding

LOCATION: 16572...1661

OTHER INFORMATION: 10-280-326.probe

NAME/KEY: misc binding

LOCATION: 1650...1673

OTHER INFORMATION: 10-280-327.probe

NAME/KEY: misc binding

LOCATION: 1650...1673

OTHER INFORMATION: 10-280-326.probe

NAME/KEY: misc binding

LOCATION: 1650...1673

OTHER INFORMATION: 10-280-326.probe

NAME/KEY: misc binding

LOCATION: 1650...1673

OTHER INFORMATION: 10-280-326.probe

NAME/KEY: misc binding

LOCATION: 1650...1673

OTHER INFORMATION: 10-280-37

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LOCATION: (559241). (559241)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (600992). (600992)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (622708). (622708)
OTHER INFORMATION: nequals a, t,
                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (234220)...(234220)
COTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (234814)...(234814)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (309398)...(309398)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
OTHER INFORMATION: n equals a,
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LOCATION: (309418) ..(309418)
OTHER INFORMATION: n equals a,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a,
                                                                          NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
                 NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a,
                                                                                                                                     NAME/KEY: misc_feature_
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a,
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LOCATION: (674435)..(6
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                                                                                                                                                                                                                    RESULT 14
US-08-916-421B-1/C
US-08-916-421B-1/C
US-08-916-421B-1/C
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6503729
TITLE OF INVENTION: januaschii
FILE REFERENCE: P8275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT PILING DATE: 1997-08-22
PRIOR FILING DATE: 1996-08-22
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                                        52 TTCAACAGCATGGTGTGAAGCGCCGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCA 111
Gaps
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22; Indels
Mismatches
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OTHER INFORMATION: n equals a, t, c
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION:
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ORGANISM: Methanococcus jannaschii
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LOCATION: (98343). (98343)
UTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
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LOCATION: (163385). (163385)
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NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
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LOCATION: (98159). (98159)
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NAME/KEY: misc_feature
LOCATION: (98239). (98239)
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a, t,
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LOCATION: (28222)
OTHER INFORMATION: n equals a,
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LOCATION: (848I2) ..(84812)
OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCATION: (98266)..(98266)
THER INFORMATION: n equals
41; Conservative
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Matches
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Search completed: August 10, 2004, 21:58:15 Job time : 14.9751 secs
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67.9%;
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INFORMATION FOR SEQ 1D NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 595 base pairs
TYPE: nucleic acid
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Best Local Similarity 67.99
Matches 38, Conservative
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Pred. No. 91;
0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 87, Application US/08976259
Patent No. 6316609
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1569020). (1569020)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1602912). (1602912)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1603734). (1603734)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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NAME/KEY: misc feature
LOCATION: (1130881).(1130881)
OTHER INFORMATION: n equals a,
                                                                  LOCATION: (1096846) .. (1096846)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (1119881) .. (1119881)
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OTHER INFORMATION: n equals a,
NAME/KEY: wisc features a,
LOCATION: (1349491)...(1349491)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
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Best Local Similarity 55.9%;
Matches 52; Conservative
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ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Ave, N.W., Suite 600 CITY: Washington STATE: DC

142

NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:

Patent No. 6316609

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95 ATTAAAATTAAAATGTCATAAACTCCTGCAAGGTGGCAAATTCCTCAAGAATAT 150
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Pred. No. 3.5;
0; Mismatches 18; Indels
                                                                                                                                          SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGIGTRATION NUMBER: 1488.0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nu	nucleic search, using sw model
Run on:	August 10, 2004, 17:10:22 ; Search time 601.675 Seconds (without alignments) 10877.634 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-001-857-41 151 1 cogccogggcaggtacctaagcaaattcctcaagaatatg 151
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 seqs, 21671516995 residues
Total number of	hits satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: 0 length: 200000000
Post-processing:	<pre>f: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</pre>
Database .	
	39: em_htgo_hum:* 40: em_htgo_mus:* 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4 5 7	ן כ	23453 Sequ	23454 Seque	61447 Human	1456 Homo sa	7452 S	AX5Z35Z3 Sequence	4869 Mils m	11473 Rattus n	08541 Rattus n	02701 Mus	2	AF272892 Rattus no	рап	Mus muscu	Hepa	Homo sap	Hepatiti	Hepatiti	Hepatiti	1	Hepatiti	Hepatiti	Hepatiti	Hepatiti	Hepariti	Hepatiti	ABIIZ408 HEDALLLIS	nepariti	3960 Henatit	320 Panio anu	126	325702	F325703 Hepatiti	01 Cae	3471 Homo sapi	1136 Hepatı	SIS79 Novel ge	SEBYZ HOMO Sap	4 Human UN	ON HOMO Sap	ZO HOMO	1798 Mus mus	AP003782 Homo sapı	
COMMENTED		234	AX52345	AL16144	AL16145	AX53745	AX5235	AC13486	AC11147	AC10854	AY10270	BC0564	AF27289	BC05328	AC102010		AC073095		AF27657	AF27657	4 AF276572		AF27657		4 AF276576	AF37879	AY21737	AB11240		4 Arues/56	AC146320	_	4	4 AF32570	_	AC073471	4 AY251	BD181	ABUSB6	HSV311	AP0035	AC025120	O ACLZ3	AP00378	
ن ب ا	Length DB	21	3096	115	20902	488	815 6	1039	53611	861	2552	594	543	467		3215	276	Н	Н	H	Н	Н	Н	н :	Η,	465 I	202	7 P T	1 1 2 1 2	-	70540	181792 9	Н	512 1		9994	994		15/5	23631	61078	1286 2	68467 I	80303	
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	Score	in	140.4	90	90	4	83.8	2	10	0	7	7	ω.	23	N	36.6	ů.	35	35	35	32	35	35	35	35	35	 	υ. υ.	υ . υ .	3. U. E.	۸,	34.8	4.	4.	4.	4.	m	33.8	'n,	m,	m i	m,	· ·	•	
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ALIGNMENTS

PAT 24-OCT-2002					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo.			genes and	
linear					Vertebrata	i; Hominidae		', Y. and Liu	ng specific	
DNA	.88.				raniata;	atarrhin		.Y., Sun	ng to lu	
151 bp	W0020647				data; C	nates; Ca		Chen, S	s relatin	
	Sequence 41 from Patent W002064788. AX523453	AX523453.1 GI:24412349	ns (human)	ns	Metazoa; Chor	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C.	ns and methods	
AX523453	Sequence 4	AX523453.1	Homo sapiens (human)	Homo sapiens	Eukaryota;	Mammalia;	-1	Macina, R.A	Compositio	proteins
RESULT 1 AX523453 LOCUS	DEFINITION	VERSION	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	

JOURNAL

FEATURES

ORIGIN

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Submitted the Tharka. 2002, Wellow First Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone amen. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one Mil subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
droup.
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/Chip
http://www.sanger.ac.uk/HGP/Chip
RP11-379P1 is from the library RPCI-11.2 constructed by the group
of Fieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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be approximately 200bp by restriction digest data."
129108
                                                                                                                                                                                                                                       Direct Submission
Submitted (16-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Tandem repeat. Forced join. Gap size estimated to be approximately 300bp by restriction digest data."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RPI1-379P1 The true left end of clone RPI1-280P22 is at 137145 in this sequence. The true right end of clone RPI1-65C15 is at 38497 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11.2"
complement(32505. .32575)
/note="Sequence from uni-directional dGTP big dye
terminator reads only."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(74706. .74920)
/note="Sequence from uni-directional dGTP big dye
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70.5%; Score 106.4; DB 9;
Best Local Similarity 99.1%; Pred. No. 4.6e-23;
Matches 107; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74706. .74920 /note="Single clone region.
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/note="Single clone region.
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1. .160115
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="9"
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            AL161447.20 GI:19572746
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 02064788-A 41 22-AUG-2002;
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Diadexus, Inc. (US)
Location/Qualifiers

    151
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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                                           35038 CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGA 34979
                                                                                                                                                                                                           AL161456 320902 bp DNA linear HTG 15-JAN-2002
Homo sapiens chromosome 9 clone RP11-85C21, 85 unordered pieces.
AL161456
                   69
                                                                                                                                                                                                                                                                                                                                                           Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5 Sequencing vector: M13, M77815; 1$ of reads Sequencing vector: plasmid; 10872; 98$ of reads Chemistry: Dye-terminator Big Dye; 100$ of reads Consensus quality: 289121 bases at least Q40 Consensus quality: 300401 bases at least Q30 Consensus quality: 306412 bases at least Q30 Insert size: 312502; sum-of-contigs Q20 Insert size: 179280; 3.8% error; agarose-fp Q40 Q4011ty coverage: 3.24% in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 85 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                             34978 AGCGCTGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATAAACT 34931
                                                                                            70 AGCGCCGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATAAACT 117
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3: contig of 2850 bp in length
3: gap of 100 bp
4: contig of 2861 bp in length
5: gap of 100 bp
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2535: gap of 100 bp
9914: contig of 7379 bp in length
00014: gap of 100 bp
4224: contig of 4210 bp in length
4324: gap of 100 bp
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of 4059 bp in length
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gap of 100 bp
contig of 5606 bp in length
gap of 100 bp
contig of 2097 bp in length
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HTG; HTGS PHASE1; HTGS CANCELLED.
Homo sapiens (human)
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18483: gap of 100
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Primates;
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Mammalia; Eutheria;
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AL161456/c
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261433 CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGA 261374
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                           Lal, P.G., Baughn, M.R., Yao, M.G., Walia, N.K., Elliot, V.S., Xu, Y.,
Honchell, C.D., Yue, H., Ding, L., Gietzen, K.J., Ison, C.H., Lu, D.A.
Hafalia, A.J., Ghandi, A.R., Thangavelu, K., Sanjamala, M.M.,
Tang, Y.T., Ramkuma, J., Griffin, J. A., Swarnaker, A., Aziman, Y.,
Sapperstein, S.K., Burford, N., Lee, B.A., Lu, Y., Tran, U.K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGA
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                                             261373 AGGCTGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATAAACT 261326
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Molecules for disease detection and treatment
Patent: WO 02070709-A 23 12-SEP-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="unassigned_DNA"
/db_xref="taxon:9606"
/note="Incyte_ID_No: 7111920CB1"
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88.5%; Pred. No. 2.6e-16;
ive 0; Mismatches 12;
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Diadexus, Inc. (US)
Location/Qualifiers
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WO02064788.
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Sequence 23 from Patent W002070709.

    11. 815
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/organism="Homo sapiens"
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AX523523
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Homo sapiens
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92; Conservative
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Matches 9
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AX537452/c
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Pred. No. 5e-23;
0; Mismatches 1; Indels
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of 2691 bp in length
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Best Local Similarity 99.1'
Matches 107; Conservative
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Query Match Best Local Matches 9

gg à AK025266/c LOCUS DEFINITION ACCESSION VERSION

RESULT 7

ORGANISM

REFERENCE AUTHORS

KEYWORDS SOURCE

JOURNAL REFERENCE

TITLE

AUTHORS

TITLE JOURNAL

COMMENT

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281804 bp DNA linear HTG 01-MAR-2003 Mus musculus chromosome UNK clone RP23-137C6, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                         Submitted (01-OCT-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 281804) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (01-MAR-2003) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 281804)
                                                                                  10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkway, St. Louis, MO 63108, USA
On Mar 1, 2003 this sequence version replaced gi:27877434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-primer ET; 04 of reads
Chemistry: Dye-primer ET; 04 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 278252 bases at least Q40
Consensus quality: 279551 bases at least Q20
Insert size: 171000; agarose-fp
Insert size: 282542; sum-of-contigs
Quality coverage: 15.67 in Q20 bases; sum-of-contigs
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1174: gap of unknown length
2325: contig of 1151 bp in length
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Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRAFT; HTGS_FULLTOP
                               13;
  Pred. No. 8.2e-16;
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Sequencing vector: M13; 0%
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McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Waterston, R.H.
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HTG; HTGS PHASE1; HTGS DRA
Mus musculus (house mouse)
  87.5%;
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                               91; Conservative
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Submitted (01-MAR-
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  Best Local Similarity
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AUTHORS
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TITLE
                               Matches
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REKVNKAAVFEEEDFQSMTYGFKMANSVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEE
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NSLHHGIQAQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLID
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VADLASFVSPPVLSPKCYLYNNHQAKDCIDSFVTHCVRPFCSLLQIHGHNRARQRDKL
GHILDEFATLQDBABKVDAALHTMLLKQEPQRQHLAMLGTWVLYHNLRIMIQYLLSGF
ELELYSMHEILLHHILVSL"
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LGELLHDKLFGLFEAMSAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTL
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Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan. (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                   87 AGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGAA 146
                                                                                                              11 AGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Nakancto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO, human, cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                           Gaps
                                                           ·;
     Length 815;
                                                                                                                                                                                                                                                                                                                                                                                              AAV25266 1839 bp mRNA linear
Homo sapiens cDNA: FLJ21613 fis, clone COL07381.
AK025266
                                                        12; Indels
                                                                                                                                                                                                                    71 GCGCCGCATCAACCTTCTCCCTATTAAATAAAATGTCATA 113
147 GCGCTGCATCAACCTTCTCTGCCTCATCCTGCAAGTGGCAAA 189
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/note="cloning vector pME18SFL3"
     DB 6;
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Homo sapiens (human)
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Score 83.8; DB 6;
Pred. No. 4.8e-16;
0; Mismatches 12,
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/db xref="GI:10437745"
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xref="taxon:9606"
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        55.5%;
                               88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1 to 1839)
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                                                           91; Conservative
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                               Similarity
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SOUTCE

FEATURES

CDS

Length 1839;

6

DB

Score 83.2;

55.1%;

Query Match

ORIGIN

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Gaps
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48.1%; Score 72.6; DB 2; Length 281804;
Best Local Similarity 85.3%; Pred. No. 4.1e-12;
Matches 81; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                            14581: contig of 4037 bp in length 14681: contig of 2244 bp in length 17225: contig of 2544 bp in length 17325: gap of unknown length 17325: gap of unknown length 22780: contig of 5455 bp in length 34746: contig of 11866 bp in length 34746: contig of 11866 bp in length 34746: gap of unknown length 51109: contig of 16263 bp in length 51209: gap of unknown length 65088: contig of 18699 bp in length 85189: contig of 18181 bp in length 85289: gap of unknown length 119762: contig of 18181 bp in length 119762: contig of 18181 bp in length 119762: gap of unknown length 119862: gap of unknown length 119862: gap of unknown length 119762: contig of 18181 bp in length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119762: contig of unknown length 119763: contig of unknown length 119763: contig of unknown length 119763: contig of unknown length 119763: contig of unknown length 119763: contig of unknown length 119763: contig of unknown length 119763: contig of unknown length 119763: contig of unknown l
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g of 3414 bp in length
f unknown length
of 4037 bp in length
f unknown length
g of 2544 bp in length
f unknown length
g of 5455 bp in length
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f unknown length
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190805: gap of unknown length
281804: contig of 90999 bp in length
                                                      length
bp in length
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note="assembly_name:Contig10"
1175. .2325
note="assembly_name:Contig12"
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/note="assembly_name:Contig38"
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note="assembly_name:Contig27"
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note="assembly_name:Contig30"
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note="assembly_name:Contig31"
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note="assembly_name:Contig33"
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note="assembly_name:Contig34"
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note="assembly_name:Contig35"
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note="assembly_name:Contig40"
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note="assembly_name:Contig32"
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                                                                                  of 2657 bunknown ]
                                                      unknown
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
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14581:
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RS MURITY, DANAILE, MEZENE, LEEE, Abranzon, S., Adams, C., Alder, J., Allan, H., Alsproofs, S., Amin, A., Auguiano, D., Allan, T., Alsproofs, S., Amin, A., Auguiano, D., Haylabero, C., Allan, H., Alsproofs, S., Amin, A., Auguiano, D., Bandarie, Mezzer, M., Barnstead, W., Barnstead, W., Barnstead, W., Barnstead, W., Barden, H., Baldwin, D., Bandaranake, D., Bander, W., Barnstead, W., Berahmed, F., Baldwin, D., Bandaranake, D., Cheng, C., Cheng, T., Coleson, E., Chu, J., Clavez, D., Chen, G., Chen, Y., Cheng, T., Chavez, D., Chen, G., Chen, Y., Chen, Y., Carter, K., Cavazo, I., Cesar, H., Center, A., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chavez, D., Chen, G., Chen, Y., Chen, Y., Carter, K., Cavazo, I., Cesar, H., Center, A., Chavez, D., Chen, G., Chen, Y., Chen, H., Elagan, A., Duth, H., Diyan, Rocha, S., Dany, Carter, K., Carter, M., Guser, M., Dayan, Rocha, S., Dany, Carter, M., Chere, T., Escotto, M., Elagan, A., Duth, H., Diyan, R., Eraser, C., Garter, R., Garter, M., Gavera, M., Gunarathe, P., Havlak, P., Haves, A., Hanlak, W., Garner, T., Garza, M., Gunarathe, P., Havlak, P., Haves, A., Handle, M., Gurner, T., Garza, M., Gunarathe, P., Havlak, P., Haves, A., Handle, S., Hamilton, C., Hamilton, K., Hernandez, R., Havlak, P., Haves, A., Hander, M., Gunarathe, P., Havlak, P., Haves, A., Hander, C., Hamilton, K., Havlak, P., Haves, A., Hunk, S.L., Hongson, A., Hogues, M., Joseber, M., Joseber, M., Johnson, L., Jacodh, M., Lohnson, B., Johnson, R., Kargi, C., Karft, C., Lebon, L., Jang, H., Vannar, M., Mannud, M., Malloy, K., Marju, M., Mannud, M., Malloy, K., Marju, M., Mannud, M., Mallow, M., Mayan, M., Morris, S., Morris, S., Morris, S., Morris, S., Morris, S., Murida, P., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, K., Martin, S., Patk, K., Martin, K., Martin, S., Patk, K., Martin, S., Patk, K., Martin, S., Patk, K., Martin, S., Patk, K., Martin, S., Patk, K., Martin, S., Patk, K., Martin, S., Patk, K., Martin
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                     241394 AGGGCTGCATCAACCTTCTCTGCCTGTCAAAACAA 241360
                                                                                                                                                                                                                                                                                                                       AC111473 AC111473 AC111473.5 GI:30579365
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus
Rattus norvegicus
70 AGCGCCGCATCAACCTTCTCTGCCTATTAAATAA 104
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2 (bases 1 to 253611)
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Direct Submission

10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGA

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                                                                                                                                          Direct Submission

L Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:24942245.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 242469 bases at least Q40
Consensus quality: 245181 bases at least Q30
Consensus quality: 246854 bases at least Q20
Estimated insert size: 222908; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250191: contig of 250191 bp in length 250291: gap of unknown length 252060: contig of 1769 bp in length 252160: app of unknown length 253161: contig of 1451 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- Genome Center
Center: Baylor College of Medicine
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clone_end:T7"
                                                                                       3 (bases 1 to 253611)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Atlas 3.0;
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/db_xref="taxon:10116"
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1. .253611
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De l (Dases 1 to 271861)

Muzny, D. Marie., Merzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalabenti, V., Aoyagil, A., Aoyagil, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Bryant, M., Blanke, D., Barber, M., Barnstead, M., Center, A.,
Cactenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Cardenad, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., L., Davis, C., Davo, Carroll, L., De Anda (C., Decarich, D.)
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Bann, Escotto, M., Edgag, M., Forbes, L., Fang, F.,
Fernandez, S., Finley, M., Elagy, M., Farser, C., Farser, C.,
Fernandez, S., Finley, M., Elagy, M., Garrer, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Garrer, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Garrer, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Garner, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Garber, M., Hognes, M., Harnandez, R., Hands, S., Hadu, S.L., Hodgson, A., Henandez, J.,
Harrandez, R., Hines, S., Hadu, S.L., Hodgson, A., Hogres, M., Jackson, L., Jackson, L., Jang, H., Levan, J., Lewis, L., Liu, W., Mahindarle, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, S., Manders, M., Marken, M., Mahneshwari, M., Martin, K., Martin, R., Marken, M., Marken, M., Marken, M., Marken, M., Marken, M., Marken, M., Marken, M., Marken, M., Morris, S., Munidasa, M., Marken, M., Morris, S., Munidasa, M., Marken, M., Morris, S., Musha, M., Morris, S., Musha, M., Morris, S., Musha, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morr
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Rattus norvegicus clone CH230-137C13, WORKING DRAFT SEQUENCE, 7
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                         Gaps
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Length 253611;
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HTG; HTGS PHASE1; HTGS_PRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Score 70.6; DB 2;
Pred. No. 1.8e-11;
0; Mismatches 34;
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          46.8%;
72.8%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23123542.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department
Submitted (31-JAN-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 271861)
Rat Genome Sequencing Consortium.
Assembly programs. Atlas 3.0; Consensus quality: 233080 bases at least Q40 Consensus quality: 23701 bases at least Q30 Consensus quality: 23701 bases at least Q20 Estimated insert size: 241904; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocontig of 4170 bp in length contig of unknown length contig of 171341 bp in length gap of unknown length contig of 6444 bp in length contig of 6324 bp in length contig of 8324 bp in length gap of unknown length contig of 1860 bp in length gap of unknown length gap of unknown length contig of 1680 bp in length contig of 1180 bp in length
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Center: Code: BCM
Center code: BCM
Web site: http://www.bgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project Information
Center project name: GJBM
Center clone name: CH230-137C13
                                                                                                                                                                                                                                                          2 (bases 1 to 271861)
Worley, K.C.
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182255:
265469:
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267349:
268529:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                    Unpublished
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182156
182256
265470
265570
267250
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175612
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JOURNAL
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97113 CAAGTICCIAAAACAGGCCAGAIGCIGICGCIGAGGCICCCIGCTICAACAACAIAGIGIGG 97172
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Mus musculus embryonic growth-associated protein EGAP mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 AGCGCCGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATAAACTCATCCTGCAAGG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (Dases 1 to 2552)

Wenzlau,J.M. and Weiser-Evans,M.C.M.

Mouse Embryonic Growth Associated Protein (EGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse bmc.,
Mopublished
Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 CAGGTACCTAAACAGGCCAAATGTTGCCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 271861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Indels
0 268629: gap of unknown length
0 271861: contig of 3232 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70.6; DB 2;
Pred. No. 1.8e-11;
0; Mismatches 34;
                                                                                                                                                                              organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                          1. .1466
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complement (3254. .3667)
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4271. 5454
Anote="wgs contig"
21028. 22738
Anote="wgs contig"
175712. 176921
Anote="wgs contig"
182256. 183591
Anote="wgs_contig"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="11"
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55. .2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site: EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.8
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97233 AGACA 97237
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268530
268630
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REKVNKAAVFEBEDPÇSMYTGFKMANSYTDLRVTGMLKOVEDDLQRRVKSTRSRQGEE
RDPFWELEHQCLAARSRVKFTRYLLIVLIAPTKKETSAVARAQKLWYQAADLLSAIH
TSLHHGIQAQNGTTKGDHPIMMGFEDLVNQRLLPPTFPRXAKIIKREEMVNYFSRLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 124 Row: k Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21644570. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKTYCEVVILPNIHOLILDFFCEFSEQSPČVISRSLLQTTFLVDNKKVFGTHLMQDMV
RIALRSFVSPPVISPROKTVNHQAROTIDSPYHCVRRPFOSIVVQIHARRARQEDKU
GHILDEFRATLQDEARKVDAALHTMLKQEPQRQHLACUGTWULYHNLRIMIQKLLSGF
ELELYSMHBYYYIYWYLSEFLYAWLMSTLSRAOGSQMAEERIMEEQQKGRSSKTKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVMTPPPVHYLQFKEMSDLNKYSPPQSPELYVAASKHFQQAKMILENIPNPDREVSR
                                                                                                                                                                                                                                                                         Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N(alpha) -terminal acetyltransferase. NatC
N(alpha)-terminal acetyltransferases contains MaklOp,
Maklip and MakJa subunits. All three subunits are
associated with each other to form the active complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.6%; Score 67.4; DB 10; Length 2594; ilarity 87.1%; Pred. No. 1.1e-10; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILKVAKPNFVVMKLLAGGHKKESKVPPEFDFSVHKYFPVVKLV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="embryonic growth-associated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="C57BL/6"
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                                                                                                                                                                                                                                                       info@bcgsc.bc.ca
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Les 74; Conserv
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Matches
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                                                                                                                                                                                              RDPEVELEHQCCLAAFSRVKFTRVLLTLIAFTKKETSAVAEAQKLMVQAADLLSAIH
TSLHHGIQAQNGTTKGDHPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFSRLID
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ILKVAKPNFVVMKLLAGGHKKESKVPPBFDFSVHKYFPVVKLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1526 CAGGTTCCTAAGCAGGCCAGATGTTGTCTCTGAGGCTCCTGTTTCAACAACATAGTATGA 1467
                                                                                   translation="MVMKATVDDDASGWELGVPEKMEKSSTSWVDITQDFEDACRELK/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 CAGGIACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGAGCATGGTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
'product="embryonic growth-associated protein EGAP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. Û.S.A. 99 (26), 16899-16903 (2002) 22388257
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.6%; Score 67.4; DB 10; Length 2552;
llarity 87.1%; Pred. No. 1.1e-10;
Conservative 0; Mismatches 11; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1466 AGCGCTGCATCAACCTTCTCTGCCT 1442
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Matches 74; Conserv
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BC056435.1
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                                                                                                                                               2543 bp mRNA linear ROD 15-SEP-2000 complete cds.
AF272892
1513 CAGGTTCCTAAGCAGGCCAGATGTTGTCTCTGAGGCTCCTGTTTCAACAACATAGTATGA 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="corneal wound healing related protein"
/protein id="AaF81791.1"
/db xref="G1:8926320"
/translation="MYMKAAVDDDASGWELNVPEKMEKSSTSWYDITQDFEDACRELK
IGELLHDKLFGLFEAMSAIEMMDPKMAAGMIGNQVNRKVLNFEQAVKDGTIKIKDLSL
PELIGIMDTCFCCLITWLEGHSLAQTVFTCLYIHNPDFTEDPAMSAFALGILKKCDIA
REKVNKAAAFEBEEDFQSMTYGFKMANGVTDLRVTGWLKDVEDDMQRRVKSTRSRQGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDPBVELEHQQCLAAFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSATH
TSTHHGIQQQQWTTKGDHPIMGFEPLVWQRLLPPTFRYAKIIKREEWVNYFSRLID
RIKTVCEVVNLQNHCHOLLDFFCEFSBQSPCVLSRSLLQTTFLVDNKKVFGTHLMQDMV
KDAPRSFVSPPVLSPECLINNHQAKDCIDSFYTHCVRSFCSLVQIHGHNRARQRDKL
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DLELYSMHEYYYIYWYLSEFLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKK
KKVRPLSREITWSQAYQNMCAGMFKTWVAFDMDGKVRKPKFELDSEQVRYEHRFAPFN
SVMTPPPVHYLQFKEMSDLSKXSPPPQPPELYVAASKHFQQAKMILESIPNADREVSR
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                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                       Yi,X.J., Li,X.F. and Yu,F.S.
A novel epithelial wound-related gene is abundantly expressed in developing rat cornea and skin
Curr. Eye Res. 20 (5), 430-440 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 2543)
Li,X. and Yu,F.
Direct Submission
Submission The Schepens Bye Research, 20 Staniford
Street, Boston, MA 02114, USA
Location/Qualifiers
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Pred. No. 2.5e-09;
0; Mismatches 28
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                                                                         AGCGCTGCATCAACCTTCTCTGCCT 1429
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/db_xref="taxon:10116"
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ilarity 74.1%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cypriniformes; Danio.

1 (Dases 1 to 2467)

2 (Stausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Munny, D.M., Sodergen, E.J., Lux, Gibbs, R.A., Rahey, J., Helton, B., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Stalska, U., Smailus, D.E., Dickson, M.C., Rodriguez, A.C., Grimwood, J.S., Schmutz, M.A., Genera, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J.S., Schmutz, M., Genera, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J.S., Schmutz, M., Genera, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J.S., Schmutz, M., Genera, E.D., Dickson, M.C., Schein, J.B., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

Tissue Procurement: Leonard I. Zon, M.D.

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www.shgc.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.AG B. Consortium/Lint at: http://image.llnl.gov Series: IRAK Plate: 117 Row: n Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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Submitted (02-JUN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Danio rerio cDNA clone MGC:64157 IMAGE:6797204, complete cds.
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Codon start=1
/product="Unknown (protein for MGC:64157)"
/protein_id="AAH53286.1"
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/db_xref="taxon:7955"
/clone="MGC:64157 IMAGE:6797204"
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/clone lib="NCI CGAP_ZKid1"
/lab_host="DH10B"
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                                            BC053286
BC053286.1 GI:31418975
                                                                                                                                                                         Danio rerio (zebrafish)
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Stren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boqualavkiy, C., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Crooke, Y., Canagelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Erizhugh, W., Galagan, J., Gardyna, S., Faro, S., Farzia, P., Fitzhugh, W., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Gardora, S., Karatas, A., Kalls, C., Lanocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marthes, C., Macdonald, P., Major, J., Marthes, C., Macdonald, P., Major, J., Marthes, S., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Compor, T., O'Donnell, P., O'Nonnell,                                                                                                                                                                                                                IKSVCEVINITNLHSILDFFCEFSEQSPČVLSRSLLQTTFLIDNKKVFGTHLMQDMIK
DALRCFVSPSPVLSSKCSLNNNHQARVTIDSFVTHCRPFPCZALQIHGHRARQRDKLG
HILEBFATLQDEAEKTVDAALHGLLMKLEPQRGHLACLGTWILYHNLRINGYLLSGFE
LELYSMHSYYYIVWYLSEFLYAWLMSTLSRADSSQMAEERILEEQLKVRSSKKSKKKK
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Mus musculus clone RP24-531M24, WORKING DRAFT SEQUENCE, 7 unordered
                               GELLHDKLFGLFEAMSAIEMMDPKMDAGMIGNQVNRKVINFDQAVKDEAIRVKDLSIP
ELIGIMDTCFCCLITWLEGHSLAQTVFTCLYVHNPDLIQDPALKAFALGILKICDIAR
                                                                                                         EKVNKAAVFEEEDFQAMTYGFKMANNVTDLRVTCMLKDVEDELQRKVKSTRSRQGEQR
DPEVELDHQQCLALFSRVKFTRLLLSALISFTKKETSAVSBAQKLMSQAADLLPAVHA
TIQYGIQSQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFSKLIER
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VVTPPPVHYI QFKEMSDLKKYNPPPRSADLYMAASKHFQQAKLLLENVTSPDAEVNRI
translation="MVMKSSVEEEEGGWGLGIPEKMRNNANWVDVTQEFKGACKELKI"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 147876)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Mak10; Region: Mak10 subunit, NatC
N(alpha)-terminal acetyltransferase. NatC
N(alpha)-terminal acetyltransferases contains Mak10p,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Indels
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Mus musculus (house mouse)
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Best Local Similarity
Matches 65; Conserv
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Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Boduslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cooke, B., Carum, B., DeArellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S.,

Grand-Pierre, N., Hafez, N., Hagoslan, D., Hagoslan, J.,

Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Inndblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,

Macdonald, P., Major, J., Manming, J., Matthews, C., McCarthy, M.,

Maldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,

Nguyen, C., Nicol, R., Mihova, T., Menga, V., Murphy, T., Naylor, J.,

Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Domell, P.,

Nowal, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schauer, S., Schupbsck, R., Seaman, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Talamas, J., Tasfaye, S., Theodore, J., Topham, K., Travers, M.,

Vassiliev, H., Venkataraman, V. S., Viell, R., Vo, A., Wilson, B.,

Nyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (21-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 21, 2003 this sequence version replaced gi:28412092.

All repeats were identified using RepeatMasker:

Smit, A. R., & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RN/RepeatMasker:html
                                                                                                                       Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
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gap of 100 bp

contig of 2353 bp in length

gap of 100 bp

contig of 2422 bp in length

gap of 100 bp
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contig of 16318 bp in length
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0; Gaps
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10.147876: contig of 28822 bp in length.
Location/Qualifiers
1..147876
| Lordanism="Mus musculus" |
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Search completed: August 11, 2004, 01:34:02 Job time : 605.675 secs

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1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbesgesc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
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	and	d Chemical	al Rese hiro-ch	arch	, Genomic	ences Center (GSC); Kanadawa 230-0045, Japan

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3071 bp mRNA linear HTC 20-SEP-200 Mus musculus 9 days embryo whole body cDNA, RIKBR full-length enriched library, clone:D03002N24 product:CORNEAL WOUND HEALING RELATED PROTEIN homolog (Rattus norvegicus), full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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0; Mismatches 2; Indels
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                            /organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="RP43-052K19.T7"
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

IN Mature 420, 563-573 (2002)

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Radachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,

Hayashida, K., Hayatsu,N., Hiramocto,K., Hiraoka,T., Hirozane,T.,

Hayashida, K., Hayatsu,N., Hiramocto,K., Hiraoka,T., Katoh,H., Kawai,J., Konda,M.,

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Ohno,M., Ohaco,M.,

Koya,S., Tangami,M., Tangawa,A., Sahingawa,A., Shiraki,T.,

Sogabe,Y., Tanaka,T., Tomaru,A., Takahashi,F., Takaku-Akahira,S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,

Muramatsu,M. and Hayashizaki,Y.
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The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
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                                                                       Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [Rattus norvegicus] (SPTR|Q9J101, evidence: FASTY, 96.2%ID, 43.5%length, match=948)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-92222
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3071;
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URL.http://genome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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57.5%; Score 86.8; DB 11;
Best Local Similarity 81.0%; Pred. No. 5.8e-17;
Matches 115; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FANTOM_DB:D030020M24"
/db_xref="MG1:2418664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev stage="9 days embryo"
1. .3071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
clone="D030020M24"
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/strain="C57BL/6J"
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96

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CESO00418 Bos taurus skin cDNA library Bos taurus cDNA clone CCCL000418 5', mRNA sequence.
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Wang, Y.H., McWilliam, S. and Lehnert, S.

Transcription profiling of cattle skin
Unpublished (2003)

Contact: Dr Yonghong Wang
Functional Genomics Lab

Functional Genomics Lab

CSIRO Livestock Industries

Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St.Lucia QLD Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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                                                                                                                                                                                                   730 ccringggricnigricaacagcargagargagagagargaaccarcaaccricragaar 671
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                                                                                                                                                         37 CTTTGGGGTTCCTGTTTCAACAGCATGTGAAGCGCCGCATCAACCTTCTCTGCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Bos taurus skin cDNA library"
/note="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcoRI;
Site 2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                 0 ;
                                         Score 75.2; DB 14; Length 812;
Pred. No. 2.5e-13;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.9%; Score 73.8; DB 14; Length 472; 91.8%; Pred. No. 6.3e-13; live 0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Adult"
/lab_host="XL1-BlueMRF'strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL000418"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="pooled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           row: D column: 09 Location/Qualifiers
                                                                                                                                                                                                                                                                                                  97 TAAAATAAAATGTCATAAACT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF762228.1 GI:37711446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
                                                  49.8%;
95.1%;
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Best Local Similarity 91.8%;
Matches 78; Conservative
                      Ouery Match
Best Local Similarity 95.1.
Best Total Similarity 77; Conservative
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Bos taurus
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CF762228/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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BI537770/c
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AUTHORS
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JOURNAL
COMMENT
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DRIGIN
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This is a long-transcript enriched cDNA library (Genome Res. II: 153-1558 (2001). [PMID: 11544199] from WAO1 cell line. Undifferentiated human ES cell line WAO1 cell line. Undifferentiated human ES cell line WAO1/HI was obtained from WiCell Research Institute, Inc., Madison, Wi, oultured according to their instructions, on MEF feeders. They formed coroning to their instructions, on MEF feeders. They formed colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EDMSE. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIECO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRI20l Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199]) bouble-stranded cDNAS were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to Lone-linker Li-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and centricon-100 column. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pCWV-SPORT6 plasmid vector. The average insert size is about 3.6kb."
                                                                              EST 18-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Irene Ginis and Mahendra Rao, NIA CDNA Library Preparation: Yulan Piao and Minoru Ko CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library (Long)"
                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
II (bases 1 to 812)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                           CD654321
AGENCOURT 14553680 NIA Human H1 Embryonic Stem Cell cDNA Library (Long) Homo sapiens cDNA clone IMAGE:30428535 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Embryonic Stem cells"
/cell_line="WAO1"
/lab_host="DH10B_(T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
Plate: NDAMS17 row: 1 column: 16
High quality sequence stop: 683.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="IMAGE:30428535"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                     CD654321.1 GI:31893486
                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                   sapiens
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                                               CD654321/c
                                                                                                    DEFINITION
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JOURNAL
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KEYWORDS
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FEATURES

COMMENT

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69

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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tal: 402 762 4366
Fax: 402 762 4366
Exail: smitch@email.marc.usda.gov
Exail: smitch@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
vo.980904.e. Vector identified by cross_match with the -minscore 18
and -minmarch 12 options.
PCR PRIMERS
FOR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB169246 B14 bp mRNA linear EST 30-JAN-2003 VBB603020215.Rl CSEQFXN41 testes Bos taurus cDNA, mRNA sequence.
1 (bases 1 to 569)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wazy, L.Z., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laggreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Chackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 CAGGTACCTAAACAGGCCAAATGCTGCCTGTGGGGCTCCTGTTTCAACAGGCATAGTATGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bosinea; Bos.

1 (bases 1 to 814)
Adelson, D. L. and Gill, C. A.
Bovine ESTS (Adelson and Gill)
Unpublished (2003)
Contact: David L. Adelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host_"DH10g"
/clone lib="MARC 1BOV"
/clone lib="Wetcor: pCPW SPORT6; Site l: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.9%; Score 73.8; DB 12;
91.8%; Pred. No. 6.6e-13;
iive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACKWARD: GTTTTCCCAGTCACGACG
Plate: 132 row: B column: 15
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 AGGGCTGCATCAACCTTCTCTGCCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
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                                                                                                                                                                                                                                            Contact: Smith TPL
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nes 78; Conserv
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                        AUTHORS
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                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                               1 (bases 1 to 466)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, W.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 CAGGTACCTAAACAGGCCAAATGCTGCCGTGGGGGCTCCTGTTTCAACAGCATAGTATGA 219
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from day 20 and day 40
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    mRNA linear
5', mRNA sequence.
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463408 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
B1682349.
B1682349.1 GI:15635283
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                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
FO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
BI537770
427999 MARC 4BOV BOS taurus CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
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                                        BI537770
BI537770.1 GI:15378880
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Bos taurus
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Best Local Similarity
Matches 78; Conserv
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Bos taurus
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
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/strain="C57BL/6J"
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Best Local Similarity 85.3%;
Matches 81; Conservative (
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
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2M0182N22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0182N22 F, genomic survey sequence.
                                                                                                                                                                                                                                                              normalized Rd 1 library, sequenced 3' with M13R primer."
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                                                                                     /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 std Error: 0.00
Plate: 0182 row: N column: 22
Seg primer: CGTTGTAAAACGACGGCCAGT
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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'strain="C57BL/6J"
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/clone="UUGC2M0182N22"
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                                                                           organism="Bos taurus"
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                   Email: david.adelson@tamu.edu.
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                                    Location/Qualifiers
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Fax: 801 585 7177
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Fax: 9798456970
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwMp42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli Xni0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF179099 974 bp mRNA linear EST 31-OCT-2000 601808136F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4038945 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 974)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.g column: 10
High quality sequence stop: 662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGA
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Pred. No. 1.6e-12;
0; Mismatches 14; Indels 0
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ORIGIN

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BB727790 BIKEN full-length enriched, 8 cells embryo Mus musculus cDNA clone E860029E01 3', mRNA sequence.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
              380 CAGGITCCIAAGCCAGAGCCAGATGITGTCTCTGAGGCTCCTGTTTCAACAACATAGTATGA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-reseges riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare [Inl-length cDNA libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y., Kira,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="8 cells"
/dev_stage="8 cells embryo"
/clone_lib="RIKEN full-length enriched, 8 cells embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'clone="E860029E01"
                                                                                                                                                                        320 AGCGCTGCATCAACCTTCTCTGCCT
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                                                                                                                           70 AGCGCCGCATCAACCTTCTCTGCCT
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB727790.1 GI:16111065
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                                                                                                                                                                                                                                                                                                       RESULT 11
BB727790/c
                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 409)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 16-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ubl5b06.rl Stratagene mouse macrophage (#937306) Mus musculus cDNA clone IMAGE:1367027 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              500 CAGGITCCTAAGCAGGCCAGAIGTIGTCTCTGAGGCTCCTGTTTCAACAACATAGTATGA 441
                                                                                                                                                                                                                                                                                                                                                                              69
                      Primer: Oligo dT
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Site_2: NotI, cloned unidirectionally. Primer: Oligo dI
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                          10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTA
                                                                                                                                                                                                                                                                                                       Gaps
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 409;
                                                                                                                                                                                                                            Score 68.4; DB 10; Length Pred. No. 4.1e-11; 0; Mismatches 26; Indels
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Pred. No. 7.2e-11;
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Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:1367027"
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Mus musculus (house mouse)
Mus musculus
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| Similarity 87.1%;
74; Conservative 0
                                                                                                                                                                                                                                45.3%;
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Best Local Similarity
Matches 84; Conserv
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ORGANISM

SOURCE

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS TITLE JOURNAL COMMENT

FEATURES

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DEFINITION
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E. (Dases I to 435)
S. Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,
Sagaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y., Watahiki, A., Yasunishi, A.,
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                    BB827250 RIKEN full-length enriched, mammary gland RCB-0526 Jyg-MC(A) cDNA Mus musculus cDNA clone G830046013 3', mRNA
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fulliwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                      218 CAGGTTCCTAAGCAGGCCAGATGTTGTCTCTGAGGCTCCTGTTTCAACAACATAGTATGA 159
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                  CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTA
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0
                            Length 426;
                      Score 67.4; DB 10; Length Pred. No. 7.3e-11; 0; Mismatches 11; Indels
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Mus musculus
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                            44.6%;
87.1%;
Query Match
Best Local Similarity 8/...
Best Local Similarity 8/...
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/organism="Mus musculus"

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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
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Konno,H., Fukunishi,Y., Shibata,K., Itch,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
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URL:http://genome.gsc.riken.go.jp,
Carninoi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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wagi,K., Fujiwake,S., Inoue,K., Toawa,M., Chara,E.,
Watsuhiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuuras,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RCB-0526 Jyg-MC(A) cDNA"
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RIKEN integrated sequence analysis (RISA)
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Pred. No. 7.3e-11;
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87.18;
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JOURNAL
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/dlone="IMAGE:3486246"

/tissue type="tumor, gross tissue"

/dev stage="7" months"

/dev stage="7" months"

/lab.host="bH10B"

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/clone lib="NGI_CGAP_Mam5"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Öligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,

NIH"
                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Mul-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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RCB-0527 Jyg-MC(B) cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nh.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM8522 row: b column: 07
High quality sequence stop: 478.
  visit our web site (http://genome.gsc.riken.go.jp) for
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0
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                                                                     Location/Qualifiers
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SOURCE
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BE308753/c
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AUTHORS
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                                                                     FEATURES
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Marra, M. Hillier, L. Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., La, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                    256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                            10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTA
                                                                                                                                  315 caddiriciraagcaggccagardrigicicigaggcricigriricaacaagarafga
                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Washly HMU Mouse EST Project Unpublished (1956)
Contact: Marra M/Mouse EST Project
Washlngton University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
             Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.6%; Score 67.4; DB 14; Length 512; 87.1%; Pred. No. 7.6e-11;
                                                  Indels
Score 67.4; DB 10;
Pred. No. 7.4e-11;
D: Mismatches 11;
                            Pred. No. 7.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: ETPrimer
High quality sequence stop: 344.
Location/Qualifiers
                                                                                                                                                                                                        255 AGCGCTGCATCAACCTTCTCTGCCT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:367891"
                                                                                                                                                                              94
                                                                                                                                                                              70 AGCGCCGCATCAACCTTCTCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="unknown"
        Query Match
Best Local Similarity 87.1%;
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             W54490.1 GI:1355550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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        Matches
        74;
        Conservative
        0;
        Mismatches
        11;
        Indels
        0;
        Gaps
        0;

        QY
        10
        CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTTCAACAGCATGTGTA
        69
        69

        Db
        404
        CAGGTTCCTAAGCAGGCCAGATGTTGTCTCTGAGGCTCCTGTTTCAACAACATAGTATGA
        345
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S S

Search completed: August 11, 2004, 04:18:35 Job time : 415.913 secs

Н

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model nucleic search, nucleic

August 10, 2004, 17:10:17; Search time 60.5488 Seconds (without alignments) 10594.393 Million cell updates/sec Run on:

US-10-001-857-41

ccgcccgggcaggtacctaa......gcaaattcctcaagaatatg 151 score: Sequence: Perfect

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Geneseq_29Jan04:* Database

geneseqn2000s:*
geneseqn2001as:*
geneseqn2001bs:*
geneseqn2003as:*
geneseqn2003bs:* geneseqn2004s:* geneseqn2003cs:* geneseqn1980s:* geneseqn1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Abq75302 Human lun		Aal49929 Human mol	Abv06162 Human pro	Abv45182 Human pro	Abv36125 Human pro	Abq75372 Human lun	Abv29823 Human pro		Adc30041 Human nov	Abv15331 Human pro	Adb53632 Primary r	Abl55204 HBV subty	Aaf22296 BAC conta	Abt23617 Stabilisi	Aan60714 Sequence	Aah88704 Human DNA	Aav82684 Fulminant	Aav82693 Fulminant	Aca35581 Prokaryot	Abv32031 Human pro	Abv40970 Human pro	Aad58431 Human PAO
SUMMARIES	ΩI	ABQ75302	ABQ75303	AAL49929	ABV06162	ABV45182	ABV36125	ABQ75372	ABV29823	ABV23940	ADC30041	ABV15331	ADB53632	ABL55204	AAF22296	ABT23617	AAN60714	AAH88704	AAV82684	AAV82693	ACA35581	ABV32031	ABV40970	AAD58431
	DB	9	9	9	Ŋ	M	Ŋ	9	ιŊ	Ŋ	σ	ß	6	9	m	7	Н	4	7	7	7	Ŋ	Ŋ	6
	Length	151	3096	2488	303	439	439	815	2668	2668	3029	356	2543	3215	129021	260	3214	160755	1445	1500	1644	362	487	322101
de	Query	100.0	93.0	56.2	55.5	55.5	55.5	55.5	55.1	55.1	55.1	54.8	41.9	22.1	21.3	21.1	21.1	21.1	20.5	20.5	20.5	20.4	20.4	20.3
	Score	151	140.4	84.8	ω.	83.8	ω.			83.2	83.2	82.8	63.2	33.4	32.2	31.8	31.8	31.8		31	31	30.8	30.8	30.6
	ult No.	 ਜ	N	m	4	Ŋ	9	7	00	σ	10	11	12	13	14	15	16	17	18	19	20	21		23
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		Abt23618 Stabilisi	Aag05377 Fragment	Aaq05378 Sequence	Aat58319 DNA seque	Aas36849 Human car	Ade47543 Human car	Aal51501 Human pan	Ade86352 Human PTP	Abz39816 N. gonorr	Aca41490 Prokaryot	Aaz54048 Neisseria	Aas16091 Hepatitis	Abk29867 Wild type	Aav82692 Fulminant	Aav82685 Fulminant	Aav82690 Fulminant	Aav82694 Fulminant	Aav82697 Fulminant	Aav82686 Fulminant	Aan93072 Sequence	Aad31765 Hepatitis
1	AAT.05544	ABT23618	AAQ05377	AAQ05378	AAT58319	AAS36849	ADE47543	AAL51501	ADE86352	ABZ39816	ACA41490	AAZ54048	AAS16091	ABK29867	AAV82692	AAV82685	AAV82690	AAV82694	AAV82697	AAV82686	AAN93072	AAD31765
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	C	20.0	20.0	20.0	20.0	19	19	19	19	19.6	19	19	19	19	19	19	19.5	19	13	19	19	19
4	30.2	30.2	30.2	30.2	30.2	30	30	30	30	29.6	29.6	29.6	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4
	4.7	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Human; lung; lung specific nucleic acid; LSNA; lung specific protein; LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer; squamous cell carcinoma; gene; chromosome 9; ss. Human lung specific nucleic acid sequence SEQ ID NO:41. BP. 20-NOV-2000; 2000US-0252054P. 20-NOV-2001; 2001WO-US045080. ABQ75302 standard; cDNA; 151 (first entry) WO200264788-A2. 05-NOV-2002 22-AUG-2002. ABQ75302; RESULT 1 ABQ75302

(DIAD-) DIADEXUS INC

ΰ Liu Sun Y, Chen S, Recipon H, Macina RA,

WPI; 2002-657601/70.

New lung specific nucleic acid useful in gene therapy or as vaccines for treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous lung diseases, as well as for diagnosing, monitoring or staging these diseases.

Claim 1; Page 168; 282pp; English.

The present invention describes an isolated lung specific nucleic acid (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid sequences comprising 17 - 73 amino acids, given in ABB25873 to ABB25965; (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b); or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific protein (LSP) sequences have cytostatic activity and can be used in gene therapy and vaccines. LSNAs and LSPs are useful for diagnosing and monitoring the presence and metastasses of lung cancer in a patient. An

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antibody that specifically binds to an LSP can be used for determining the presence of an LSP in a sample, as well as for treating a patient with lung cancer, particularly by inducing an immune response against the lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs and LSPs are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-cancerous disease states in lung
      888888888888
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Sequence 151 BP; 42 A; 39 C; 32 G; 38 T; 0 U; 0 Other;

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                                                                                                                            ATGGTGTGAAAGCGCCGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATAAAACTCAT 120
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                                                             CCGCCCGGGCAGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGC
                                                                                             cceccedecrectrarecadeccaraterrecerrreseerrecretrical
                                 Gaps
                                 .
 Length 151;
100.0%; Score 151; DB 6; 100.0%; Pred. No. 3.6e-43;
                                                                                                                                                                                        CCTGCAAGGTGGCAAATTCCTCAAGAATATG 151
              Best Local Similarity 100.0%; Pred. No. 3.6
Matches 151; Conservative 0; Mismatches
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 Query Match
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CCTGCAAGGTGGCAAATTCCTCAAGAATATG 151 121

ABQ75303 standard; cDNA; 3096 05-NOV-2002 ABQ75303; ABQ75303, RESULT

(first entry)

specific protein; Human; lung; lung specific nucleic acid; LSNA; lung

Human lung specific nucleic acid sequence SEQ ID NO:42.

LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer; squamous cell carcinoma; gene; chromosome 9; ss.

Homo sapiens

WO200264788-A2.

22-AUG-2002

20-NOV-2001; 2001WO-US045080.

20-NOV-2000; 2000US-0252054P.

(DIAD-) DIADEXUS INC.

ຜ່ Sun Y, Ś Chen Recipon H, Macina RA,

WPI; 2002-657601/70.

New lung specific nucleic acid useful in gene therapy or as vaccines for treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous lung diseases, as well as for diagnosing, monitoring or staging these diseases

Claim 1; Page 168-169; 282pp; English.

The present invention describes an isolated lung specific nucleic acid (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid sequences comprising 17 - 733 amino acids, given in ABP52873 to ABP52955; (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp) given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b), or (d) has 60 % sequence identity to (a) or (b). LSNA and lung specific protein (LSP) sequences have cytostatic activity and can be used in gene therapy and vaccines. LSNAs and LSPs are useful for diagnosing and monitoring the presence and metastases of lung cancer in a patient. An

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antibody that specifically binds to an LSP can be used for determining the presence of an LSP in a sample, as well as for treating a patient with lung cancer, particularly by inducing an immune response against the lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs and LSPs are useful for identifying, diagnosing, monitoring, staging,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human molecules for disease detection and treatment (MDDT), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant MDDT expression, e.g. cancer, AIDS, asthma, diabetes, hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                  imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-cancerous disease states in lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; molecule for disease detection and treatment; MDDT; gene therapy cytostatic; antiatreriosclerotic; hepatotropic; anti-HIV; antiallergic; anti-HIV; antiallergic; anti-HIV; antiasthematic; cerebroprotective, nootropic; neuroprotective; antiparkinsonian; cardiant; antianginal; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 AGGGCGGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATAAACTCATCCTGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human molecule for disease detection and treatment coding sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2052 CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                            10 CAGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTAA
                                                                                                                                                                                                                                                                                                                                                                Gaps
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MM, Tang YT;
Sapperstein SK;
                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                        Length 3096;
                                                                                                                                                                                                                                             Sequence 3096 BP; 914 A; 606 C; 749 G; 827 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu X;
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Ding L, Gietzen KJ, Ison CH, Iu
AR, Thangavelu K, Sanjanwala MM,
JR, Swarnaker A, Azimzai Y, Sapp
Lu Y, Tran UK, Marquis JP;
                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                                       6.9e-39;
                                                                                                                                                                                                                                                                                                                           99.3%; Pred. ...
                                                                                                                                                                                                                                                                                                     93.0%; Score 140.4; 99.3%; Pred. No. 6.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCAAATTCCTCAAGAATATG 1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
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2001US-0271118P.
2001US-0274486P.
2001US-0274436P.
2001US-0334229P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL49929 standard; cDNA; 2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2002; 2002WO-US003709.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                Matches 141; Conservative
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Honchell CD, Yue H
                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-713453/
P-PSDB; AAO19400
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23-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2002;
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Burford N,
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                                                       molecules for disease detection and treatment MDDT. The sequences can be used in the treatment of diseases associated with the decreased expression or overexpression of MDDT, such as cell proliferative (cancer, atherosclerosis, hepatitis), autoimmune/inflammatory (e.g. AIDS, allergies, Addison's disease, asthma), developmental (dwarfism, renal tubular acidosis), neurological (e.g. stroke, Parkinson's disease, epilepsy) and cardiovascular (congestive heart failure, myocardial
                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                        infarction, angina pectoris) disorders. The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cells and correlating with presence of prostate cancer, useful
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                                                                                                                                                                                                           Sequence 2488 BP; 768 A; 461 C; 567 G; 692 T; 0 U; 0 Other;
                                            and coding
                                                                                                                                                                                                                                                                                                                                                                              1494 AGGGCTGCATCAACCTTCTCTGCTGTGCAAGTGGCGAAA 1451
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                                                                                                                                                                                                                                                                      12; Indels
                                          present invention relates to human proteins
                                                                                                                                                                                                                                       Score 84.8; DB 6;
Pred. No. 2.8e-19;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate expression marker cDNA 6153.
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               11; Page 159-160; 177pp; English.
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2000US-0211314P.
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2000US-0189862P.
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88.5%;
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Best Local Similarity
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
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progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                         Score 83.8; DB 5; Length 303; Pred. No. 2.7e-19;
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                                                                                                                                                                                   Sequence 303 BP; 81 A; 72 C; 77 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                        CTGCCTATTAAAATAAAATGTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 45173.
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2000US-0207454P.
2000US-0211314P.
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2000US-0255281P
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nes 91; Conservative
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09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                        100 AGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAA 159
                                                                                                                                                                                       11 AGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                    Gaps
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                                                                                                                 DB 5; Length 439;
                                                                          Sequence 439 BP; 113 A; 104 C; 110 G; 112 T; 0 U; 0 Other;
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                                                                                                                                                    12; Indels
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                                                                                                                                                                                                                                                                                                   160 GCGCTGCATCAACCTTCTCTGCCTCATCCTGCAAGGTGGCAAA 202
                                                                                                           Score 83.8; DB 5;
Pred. No. 3.2e-19;
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 36116.
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; 2000US-0189862P.
; 2000US-0207454P.
; 2000US-0211314P.
                                                                                                               55.5%;
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                                                                                                                               Best Local Similarity 88.3
Matches 91; Conservative
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                                                                                                              100 AGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs and LSPs are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes an isolated lung specific nucleic acid
                                                                            11 AGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; lung; lung specific nucleic acid; LSNA; lung specific protein;
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                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSP; cytostatic, gene therapy; vaccine; metastasis; lung cancer; squamous cell carcinoma; gene; chromosome 9; ss.
                                     0;
 Length 439;
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                                     12;
 Score 83.8; DB 5;
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                                     0; Mismatches
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 55.5%;
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                                     91; Conservative
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Query Match
Best Local Similarity
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Best_Local Similarity Matches 91; Conserv

Query Match

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70 AGCGCCGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATA 113
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                           AGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGAA 146
            70
                                                                                                                                                                                                                                       cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of
prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 2668 BP; 742 A; 617 C; 483 G; 820 T; 0 U; 6 Other;
                                                                       147 GCGCTGCATCAACCTTCTCTGCCTCAAGGTGGCAAA 189
                                                           GCGCCGCATCAACCTTCTCTCTCTATTAAAATAAAATGTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83.2; DB 5;
Pred. No. 1.1e-18;
0; Mismatches 13;
                                                                                                                                                                                                                     Human prostate expression marker cDNA 29814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 6420; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monahan JE;
                                                                                                                                              ABV29823 standard; cDNA; 2668 BP
                                                                                                                                                                                                                                                                                                                                                                                        2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
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l Similarity 87.5%;
91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-662795/76
                                                                                                                                                                                                                                             Human; prostate
pharmacogenomic
                                                                                                                                                                                                                                                                                                       WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy (e) selecting a composition for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2668 BP; 742 A; 617 C; 483 G; 820 T; 0 U; 6 Other;
1127 AGCGCTGCATCAACCTTCTCTGCCTCATCCTGCAAGGTGGCAAA 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacogenomic marker; gene; ss.
                                                                                                                                                                           BP
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                                                                                                                                                           ABV23940 standard; cDNA; 2668
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16-MAR-2000;
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1067 CAGGTACCTAACCAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGA 1126

CAGGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTA

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Matches

Gaps

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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a mucleic acid of the invention; the crecombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of complex of invention further discloses methods to a polypeptide of the invention. The invention further discloses methods to a polypeptide of the invention. The invention and/or monoclonal antibodies for carrying out the methods of the invention methods for the identification of compounds that modalate the expression or activity of the polymucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC31841. The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the case of data ind products dependent on DNA and amino acid sequences. They are contiguated and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's allowed the reacher's disease, and other results and products dependent on DNA and amino acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                   biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antilicer; osteopathic; immunosuppressive; antinflammatory; cytostatic;
                                                                                                                                                                                                     diagnostic; drug screening; forensics; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J,
Wang Z,
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Asundi V,
                                                                                                                                                              Human novel cDNA sequence, SEQ ID NO:123
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                                                                                                                                                                                                                                                                                                                                      gene therapy; chromosome 9; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ,
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Wang D, Ma Y,
                                         ADC30041 standard; cDNA; 3029 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT;
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                                                                                                                       (first entry)
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P-PSDB; ADC31012
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                       18-DEC-2003
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                                                                                ADC30041;
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RESULT 10
                        ADC30041
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Wehrman T; Weng G;

disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically

disease and other neurodegenerative diseases, anaemia, platelet

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The sequence data for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef
                                                                                                                                                            Gaps
              this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                            .,
                                                                                                                         Length 3029;
                                                                                      Sequence 3029 BP; 895 A; 593 C; 739 G; 802 T; 0 U; 0 Other;
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                                                                                                                                                            Indels
claimed human cDNA sequence of the invention. Note:
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thes 13;
                                                                                                                         Score 83.2; DB 9;
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                                                                                                                                        Pred. No. 1.16
0; Mismatches
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2000US-0207454P.
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2000US-0219007P.
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91; Conservative
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25-MAY-2000;
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           comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                10 CAGGIACCIAAACAGGCCAAAIGIIGCCIITIGGGGIICCIGIITICAACAGCAIGGIGIGA
compound, and comparing the gene expression profile to a database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HBV; subtype adr; surface antigen; HBsAg; core antigen; detection;
hepatitis B; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1475 AGGGCTGCATCGACCTTCTCTGCATCTTGCAAGGTGGCAAACTCT 1428
                                                                                                                                                                                                                                                       Score 63.2; DB 9; Length 2543; Pred. No. 1.2e-11; 0; Mismatches 28; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                           70 AGCGCCGCATCAACCTTCTCTCCCTATTAAAATAAAATGTCATAAACT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Surface antigen (HBsAg; AAM49180)"
                                                                                                                                                                                                                      Sequence 2543 BP; 725 A; 554 C; 627 G; 637 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product = "Core antigen (AAM49181)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /bound_moiety= "HBV capture probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= d
/note= "Primer S-03/I (ABL55208)"
complement(150. .290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "Primer S-N1/I (ABL55201)"
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'note= "Primer AS-3/I (ABL55202)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= g
/note= "Primer AS-2/I (ABL55203)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Primer AS-4/I (ABL55209)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-02/I (ABL55207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (15. .34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (60. .79)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (70. .89)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL55204 standard; DNA; 3215 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/note= "Primer
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 74.1%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29. .709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxic effect; gene expression profile; hepatotoxicity; diagnostic marker; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining if a compound induces a toxic effect on a tissue or cell, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                               71
                                                                                                                                                GGTACCTAAACAGGCCAAATGTTGCCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                               Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4174.
                                                                                                               GGTACCTAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAAG
                                                                           Gaps
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                                      Length 356;
                                                                           12; Indels
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                                                                                                                                                                                                          CGCTGCATCAACCTTCTCTGCCTCATCCTGCAAGGGGCCAAA 102
                                                                                                                                                                                     CGCCGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATA 113
 A; 80 C; 85 G; 94 T; 0 U; 0 Other;
                                      DB 5;
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                                    Score 82.8; DB
Pred. No. 6.6e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson K,
                                                                                                                                                                                                                                                                                                                    BP
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13-MAR-2002; 2002US-0353534P.
08-APR-2002; 2002US-037024BP.
10-APR-2002; 2002US-0371134P.
10-APR-2002; 2002US-0371135P.
11-APR-2002; 2002US-0371150P.
11-APR-2002; 2002US-0371413P.
19-APR-2002; 2002US-0373601P.
22-APR-2002; 2002US-0373601P.
22-APR-2002; 2002US-0373601P.
08-MAY-2002; 2002US-0373601P.
09-MAY-2002; 2002US-0373652P.
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2002US-0378665P.
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                                                                                                                                                                                                                                                                                                                  ADB53632 standard; DNA; 2543
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                                      54.8%;
88.2%;
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                   Query Match
Best Local Similarity 88.2
Best Local 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-731472/69.
 Sequence 356 BP; 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-2002;
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Elashoff
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124933 CTAGTGTCTCTTTCAACTTTCCAGTTGAAGATCCGTGTACAGGAGACTGTAAACAACCTT 124992
                                                                                                                                                                    Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                 The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAAGCGCCGCATCAACCTT
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 129021 BP; 42091 A; 22610 C; 24583 G; 39735 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     21.3%; Score 32.2; DB 3; Length 129021; llarity 59.1%; Pred. No. 5.4; Conservative 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTGCCTATTAAAATAAAATGTCATAAACTCA
                                                                                                                                                                                                                                    Claim 102; Page 686-716; 1449pp; English.
                                                                                                       Keith
     99US-0153584P.
99US-0154603P.
99US-0172493P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-2002; 2002WO-JP005832,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-2001; 2001JP-00177737.
20-AUG-2001; 2001JP-00249689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                       Copenhaver G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TAKI ) TAKARA BIO INC.
                                                                      (UYCH-) UNIV CHICAGO.
                                                                                                                                     WPI; 2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-148805/14.
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus.
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     13-SEP-1999;
17-SEP-1999;
16-DEC-1999;
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                                                                                                       Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ABT23617/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acid sequences used to detect hepatitis B virus (HBV). The invention specifically claims a sense capture probe (BABL55199) corresponding to a fragment of the surface antigen (HBSAg) coding sequence (bases 150-290 at the HBV subtype adr DNA shown in ABL55204), and to inosine-containing primers (ABL55201-ABL55202) which bind to regions of the HBV genome in or near the HBSAg coding sequence. The invention also relates to DNA molecules in which at least one base is deleted, replaced or added in the capture probe sequence, and which hybridises to HBV DNA between bases 21-710 of ABL55204, and additionally encompasses methods and reagents used in detecting HBV using the capture probe of the invention. The present sequence represents a fragment of the HBV subtype adr genome encoding the surface and core antigens used in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1679 IGAACAGACCAATITTATGCCIACAGCCTCCTAGTACAAAGACCATTAACCTAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 TAAACAGGCCAAAIGIIGCCIIIIGGGGIICCIGIIICAACAGCAIGGIGIGAAGCGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1619 ccccaacrccrccagrcrrraacaacaarcrrraaaararagccrcaaggrcg 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132
                                                                                                                                                                                                                                                                             Novel DNA used as a capturing probe for detecting hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 ATCAACCTTCTCTGCCTATTAAAATAAAATGTCATAAACTCCTGCAAGGTGG
                  /*tag= k
/note= "Corresponds to bases 1-436 of ABL55200"
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0
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Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC containing repeats from centromeres 1-4 #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                              Example 1; Page 14-16; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Centromere; michrosome; vector; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF22296 standard; DNA; 129021
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99US-0127409P.
99US-0134770P.
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                                                                                                                                                                 2000JP-00178470
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ilarity 55.7%;
Conservative (
 3215
                                                                                                                                                                                                                                                  P-PSDB; AAM49180, AAM49181.
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                 /*tag≕
 2780.
                                                                                                                                                                                              (FURE ) FUJIREBIO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                               WPI; 2002-191858/25
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                                                                 JP2001352989-A
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                                                                                                                                                               14-JUN-2000;
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01-APR-1999;
18-MAY-1999;
 misc feature
                                                                                              25-DEC-2001
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AAF22296
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Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage; specific amplification; pathogenic microorganism; chimeric; genetic engineering; clinical medicine; ss.
                                                                                                                                                                                                                                                                                                                                                                Kobayashi E;
                                                                                                                                                                                                                                                                                                                                                                                                                       Method for stabilizing and storing reaction reagents for specific amplification and detection of nucleic acids particularly in e.g. identifying pathogenic microorganisms or viruses in sample.
                                                                                                                                                                                                                                                                                                                                                               Mukai H, Yamamoto J, Tomono J,
                                                                                                                               Stabilising reagent method related oligo SEQ ID No 69.
124993 CCATGCCGAGCAGAATCAAATGTCATAAGCTGA 125025
                                                           BP.
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Example 15; Page 131-132; 177pp; Japanese.
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The invention relates to a novel stabilising reaction reagent for use in the amplification and/or detection of a target nucleic acid os comprising: preparing a reaction mixture with e.g. a nucleic acid as template, at defined pared in RNaseH; and incubation of the reaction mixture for a defined period of time to form a reaction product during the amplification of such target nucleic acid. The method is useful for stabilising and long-term storage of reaction reagents for highly sensitive and specific amplification and detection of nucleic acids particularly in identifying pathogenic microorganisms or viruses in a sample using chimeric oligonucleotide primers, which is useful in genetic engineering and clinical medicine. This polynucleotide sequence method of the invention

Sequence 560 BP; 101 A; 167 C; 143 G; 149 T; 0 U; 0 Other;

o; Gaps 0; Query Match 21.1%; Score 31.8; DB 7; Length 560; Best Local Similarity 54.8%; Pred. No. 0.84; Matches 63; Conservative 0; Mismatches 52; Indels

439 TGAACAGACCAATTTATGCCTACAGCCTCCTAGTACAAAGACCTTTAACCTAATCTCCTC 380 TAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAAGCGCCGC 1.8

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Search completed: August 10, 2004, 21:54:08 Job time : 64.5488 secs

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Sequence 296, App
Sequence 297, App
Sequence 298, App
Sequence 290, App
Sequence 291, App
Sequence 291, App
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Sequence 3218, Ap
Sequence 9543, Ap
Sequence 15927, A
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Sequence 111, App
Sequence 20725, A
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                                                                                                      August 10, 2004, 21:58:32 ; Search time 70.0822 Seconds (without alignments) 10571.835 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 290, Sequence 291, Sequence 292,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2 6/ptodata//pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata//pubpna/USO6 NEW PUB.seq:*
3: /cgn2 6/ptodata/2/pubpna/USO6 NEW PUB.seq:*
4: /cgn2 6/ptodata/2/pubpna/USO6 NEW PUB.seq:*
5: /cgn2 6/ptodata/2/pubpna/USO6 PUBCOMB.seq:*
6: /cgn2 6/ptodata/2/pubpna/USO6 NEW PUB.seq:*
7: /cgn2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*
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13: /cgn2 6/ptodata/2/pubpna/USO9 NEW PUB.seq:*
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16: /cgn2 6/ptodata/2/pubpna/USO9 NEW PUB.seq:*
16: /cgn2 6/ptodata/2/pubpna/USO9 NEW PUB.seq:*
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19: /cgn2 6/ptodata/2/pubpna/USO0 PUBCOMB.seq:*
11: /cgn2 6/ptodata/2/pubpna/USO0 NEW PUB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-814-353-9543
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US-10-467-433-23
US-10-001-857-111
US-10-98-14-353-20725
US-10-453-792-297
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US-10-453-792-291
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                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           3225727 seqs, 2453303834 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                          using sw model
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Match Length DB
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Perfect score:
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2	sequence 2349, Ap Sequence 2349, Ap Sequence 33, Appl Sequence 125454, Sequence 29360, A Sequence 2946, A Sequence 2, Appl Sequence 16, Ap
149-801A- 149-801A- 153-792-2 182-122A- 182-122A- 183-792-3 193-792-3 193-792-3 193-792-3 193-792-3 193-792-3 193-792-2 193-792-3	091.504.234 262.552.33 262.552.33 703.210.33 424.599.125 369.423.234.29 37.297.2 875.453.16
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ALIGNMENTS

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APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Pro
FILE REPERBERS DEX.-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILING DATE: 2001-11-20
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.larity 100.0%; Pred. No. 3.1e-42;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCTGCAAGGTGGCAAATTCCTCAAGAATATG 151
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/252,054
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
SEQ ID NO 41
LENGTH: 151
                     ; Sequence 41, Application US/10001857; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 151; Conserv
US-10-001-857-41
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APPLICANT: Lillite, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 Argargradaggarackarcarcricracharcracharakan
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                                                                                                                                                                                                                                                                         Length 602;
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                                                                                                                                                                                                                                                                    62.1%; Score 93.8; DB 10;
89.4%; Pred. No. 4.8e-22;
live 0; Mismatches 12;
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Pred. No. 4.8e-22;
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CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR PILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-27

PRIOR FILING DATE: 2000-07-27

NUMBER OF SEQ ID NOS: 22037

SECTAMARE: FASISEQ for Windows Version 4.0

SEQ IN NO 9543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9543, Application US/09814353 Publication No. US20030165831A1
                                                                                                                                  NAME/KEY: misc feature;
LOCATION: 561, 590;
CTHER INFORMATION: n = A,T,C or G
US-09-814-353-3218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-9543
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Matches 101; Conservative
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                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 561, 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-814-353-9543
             SEQ ID NO 3218
                                        602
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                                                                                                                                                                                                                                                    APPLICANT: Recipon, Applicants Recipon, Applicants Recipon, Applicants Recipon, Applicants Recipon, Applicants Recipon, Applicants Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot FILE REPERENCE: DEX. 2023
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT PILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1992 AGGGTGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATAAACTCATCCTGCAAGG 1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2052 CAGGTACCTAAACAGGCCAAATGTTGCCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGA 1993
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APPLICANT: Lille, Jamela
APPLICANT: Thompson, Pamela
APPLICANT: Lille, Jamela
APPLICANT: Lille, Jamela
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR PAPLICATION NUMBER: US 60/191,031
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PLING DATE: 2000-06-25
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
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PRIOR PLING DATE: 2000-12-21
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PRIOR PLING DATE: 2000-12-21
PRIOR PLING DATE: 2000-12-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; DB 14; Length 3096;
6.4e-38;
thes 1; Indels 0;
121 CCTGCAAGGTGGCAAATTCCTCAAGAATATG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 140.4; D
Pred. No. 6.4e-
0; Mismatches
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Publication No. US20030165831A1
GENERAL INFORMATION:
                                                                                                                                                       Sequence 42, Application US/10001857
Publication No. US20020183500A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.33
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                               US-10-001-857-42/c
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APPLICANT: MARQUIS, Joseph P.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
                                                                                                                                                                                                                      AMPOSITIONS, KITS, AND METHODS
I, ASSESSMENT, PREVENTION, AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: INCTE CORPORATION;
APPLICANT: IAL, Preeti G.; BAUGHN, Mariah R.;
APPLICANT: IAL, Preeti G.; CHAMLA, Narinder K.;
APPLICANT: ELLIOTT, Vicki S.; XU, Yuming;
APPLICANT: HONCHELL, Cynthia D.; YUE, Henry;
APPLICANT: DING, Li, GIETZEN, Kimberly J.;
APPLICANT: ISON, Craig H.; LU, Dyung Aina M.;
APPLICANT: HAPALIA, April J.A.; GANDHI, Ameena R.;
APPLICANT: THANGAVELU, Kavitha; SANJANMALA, Madhusudan M.;
                                                                                                                                        APPLICANT: Lee, John
APPLICANT: Lee, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPAND, CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/201,1940
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR APPLICATION NUMBER: US 60/210,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SEQ ID NO 15927
LENGTH: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TANG, Y. Tom; RAMKUMAR, Jayalaxmi;
GRIFFIN, Jennifer A.; SWARNAKAR, Anita;
AZIMZAI, Yalda; SAPPERSTEIN, Stephanie K.;
BURFORD, Nell; LEE, Ernestine A.;
LU, Yan; TRAN, Uyen K.;
                                ; Sequence 15927, Application US/09814353; Publication No. US2030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 23, Application US/10467433; Publication No. US20040087773A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-814-353-15927
US-09-814-353-15927
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US-10-467-433-23/c
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APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR PILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 111
LENGTH: 815
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Best Local Similarity 88.5%; Pred. No. 1.3e-18;
Matches 92; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No: 7111920CB1
US-10-467-433-23
                                      CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: PCT/US02/03709
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2001-02-09
PRIOR PPLICATION NUMBER: US 60/269,117
PRIOR PPLICATION NUMBER: US 60/269,618
PRIOR PPLICATION NUMBER: US 60/271,118
PRIOR PELICATION NUMBER: US 60/271,118
PRIOR PELICATION NUMBER: US 60/271,118
PRIOR PELICATION NUMBER: US 60/274,486
PRIOR PELICATION NUMBER: US 60/274,436
PRIOR FILING DATE: 2001-03-07
PRIOR PELICATION NUMBER: US 60/374,436
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: US 60/334,229
PRIOR PELING DATE: 2001-11-28
PRIOR PELING DATE: 2001-11-28
PRIOR PELING DATE: 2001-01-09
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PRIOR PELING DATE: 2001-01-09
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PRIOR PELING DATE: 2001-01-09
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CURRENT APPLICATION NUMBER: US/10/467,433 CURRENT FILING DATE: 2003-08-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (206)..(305)
OTHER INFORMATION: a, c, g or t
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapien FEATURE:
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Best Local Similarity
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ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
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US-10-453-792-296
                                                                                        COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36, 663
REFERENCE/DOCKET NUMBER: 2551-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 297, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                        FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 296:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.7;
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                              CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
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                                                                                          87 AGGTACCTAAACAGGCCAAATGTTGCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAA 146
                                                70
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                                              11 AGGTACCTAAACAGGCCAAATGTTGCCCTTTGGGGTTCCTGTTTCAACAGCATGGTGTAA
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  Gaps
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
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MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AGCGCCGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
  12; Indels
                                                                                                                                                                                  147 GCGCTGCATCACCTTCTCTGCCTCATCCTGCAAGGTGGCAAA 189
                                                                                                                                         71 GCGCCGCATCAACCTTCTCTGCCTATTAAAATAAAATGTCATA 113
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  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THILE REFERENCE: MRI-066

CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR PRILING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20725
LENGTH: 2610
                                                                                                                                                                                                                                                                                                   Sequence 20725, Application US/09814353 Ubblication No. US20030165831A1 GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 296, Application US/10453792
Publication No. USZ0040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 1, 2, 3, 4
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-20725
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                         RESULT 8
US-09-814-353-20725
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  91;
Matches
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1807 IGAACAGACCAATTIATGCCTACAGCCTCCTAGTACAAAGACCATTAACCTAATCTCCTC 1748
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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55.7%; Pred. No. 1.1;
tive 0; Mismatches 51;
                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
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NAME: SADOFF, B.J
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 ATCAACCTTCTCTGCCTATTAAATAAATGTCATAAACTCCTGCAAGGTGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3215;
                  OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.4; DB 13;
Pred. No. 1.1;
0; Mismatches 51;
                                                                                                                                            PRIOR APPLICATION: COLLALOWILL
PRIOR APPLICATION NUMBER: US/09/155,885A
PILLING DATE: 08-0CL-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 86-4000
                                                                                    APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/453,792
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 298, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 297: SEQUENCE CHARACTERISTICS:
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55.7%;
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Best Local Similarity
Matches 64; Conserva
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US-10-453-792-298/c
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1804 IGAACAGACCAATITTATGCCTACAGCCTCCTAGTACAAGATCATTAACCTAAGTTCCTC 1745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1744 CCCCAACTCCTCCAGTCCTTAAACAACAGTCTTTGAAGTATGCCTCAAGGTCG 1690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAERTENS, GEERT TILLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV NUMBER OF SEQUENCES: 313 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 21.1%; Score 31.8; DB 13;
Local Similarity 54.8%; Pred. No. 4;
Los 63; Conservative 0; Mismatches 52;
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APPLICATION NUMBER: US/10/453,792

FILING DATE: 04-Jun-2003

CLASSIFICATION: -CURCION: -
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/155,885A

FILING DATE: 08-Oct-1998

APPLICATION NUMBER: PCT/EP97/02002

FILING DATE: 21-APPR-1997

FILING DATE: 19-APR-1996
                                                                    APPLICATION NUMBER: 2996870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SALOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 298:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve-
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
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STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 298:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 290, Application US/10453792
Publication No. USZ0040029110A1
GENERAL INFORMATION:
APPLICANT: STUYVER, LIEVEN
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3212 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
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1807 realeaceaertrareceracecerecresarealacerrareales
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                                                                                                                                                                                                                                                                                                                                                                                                             78 ATCAACCTICTCTGCCTATTAAAATAAAATGTCATAAACTCCTGCAAGGTGG 132
                                                                                                                                                                                                            21.1%; Score 31.8; DB 13; Length 3215; 54.8%; Pred No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGRICIAN GERRY
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/453,792
FLING DATE: 04-JUN-2003
CLASSIFICATION: «UNKNOW»>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 19-APR-1997
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                  0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 292:
US-10-453-792-292
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REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 291:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Publication No. US20040029110A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703) 816-4100
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                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 292
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                        Similarity 54.8
63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 TAAACAGGCCAAATGTTGCCTTTTGGGGTTCCTGTTTCAACAGCATGGTGTGAAGCGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1747 CCCCAACTCCTCCAGTCTTTAAACAATACAGTCTTTGAAGTATGCCTCAAGGTCG 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 2010-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE STADERS: ABDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-JUL-2003
CLASSIFICATION OF CURROWN-
PRIOR APPLICATION NUMBER: US/09/155,885A
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-0CC-1998
APPLICATION NUMBER: EP 96870053.4
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Score 31.8;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 290: US-10-453-792-290
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REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
REGISTRATION NUMBER: 36,663
                    REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 290:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 291, Application US/10453792
Publication No. US20040029110A1
GENERAL INFORMATION:
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                                                                                                                                                                       LENGTH: 3215 base pairs
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ROSSAU, RUDI
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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54.8%;
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Best Local Similarity 54.8*
Matches 63; Conservative
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COUNTRY: U.S. VIGILALA
CONPUTER READABLE FORD
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30 (EPO)
SOFTWARE: PALENTIN NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION NUMBER: US/09/155,885A
PRIOR APPLICATION NUMBER: US/09/155,885A
PILING DATE: 19-ARR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF: B.J.
REGISTRATION NUMBER: B9 96870053.4
FILING DATE: 19-ARR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF: B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
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            DB 13; Length 3215;
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MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
                                                                                    52; Indels
        Score 31.8; DE
Pred. No. 4;
0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 295:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 295, Application US/10453792
Publication No. US200040029110A1
GENERAL INFORMATION:
APPLICANT: STUTVER, LIEVEN
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STRANDEDNESS: single
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            21.1%;
54.8%;
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 54.8°
Matches 63; Conservative
                                                                                63; Conservative
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Query Match
Best Local Similarity
Matches 63; Conserv
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US-10-453-792-295/c
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QY 78 ATCAACCTTCTGGCTATTAAATAAATGTCATAAACTCATCCTGCAAGGTGG 132

Db 1747 CCCAACTCCTCCCAGTCCTTAAACAAACGGTCTTGAAGTATGCCTCAAGGTCG 1693
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Search completed: August 11, 2004, 13:00:41 Job time: 71.0822 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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August 10, 2004, 17:10:22 ; Search time 12336.3 Seconds (without alignments) 10877.634 Million cell updates/sec 1 ttcctcacgaaactcccagg......atttcttgacaaaaaaa 3096 6940544 Total number of hits satisfying chosen parameters: 3470272 segs, 21671516995 residues - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 US-10-001-857-42 3096 Title: Perfect score: Scoring table: OM nucleic Sequence: Searched: Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

em_sts:*
em_un:*
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em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htg_pln:*
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Pred. No. is the number of results predicted by chance to have a

em_htgo_hum:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1 AX523454 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	AX523454 3096 bp DNA linear PAT 24-OCT-2002 Sequence 42 from Patent W002064788. AX523454 GI:24412350
SOURCE ORGANISM	Homo sapiens Homo sapiens Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Euthoria, Drimates, Catarrhini, Enminias, Homo
REFERENCE AUTHORS TITLE	naminary, Deficient, France Continuity, Co

TTGATAACGTGGTTAGAAGGCCATTCACTGGCACAGACAG	1081 CAGTCAATGACTTATGGATTTAAAATGGCTAACAGTGTGACGACTTCGAGTTACAGGC 1140	1201 GGAGAAGAAGAGTCAGAACTTGAACTCAGAACACCAACAATGTTTAGCAGTATTCAGC 1260	1321 AGTGCTGTTGCAGAAGCTCAAAAATTGATGGTTCAAGCAGCAGATCTTCTTTCT	CATAATTCATTGCATCATGGCATCCAGGCCCAGAATGATACTACAAAAGGAGATCATCCA ATTATGATGGGTTTTGAACCCCTTGTGAACCAGAGGCTACTTCCACCTACCT	1501 TATGCAAAATRATTAAAGGGAAGAAATGGTGAACTATTTGCAAGATTAATAGATAG	1621 TGTGAATTTAGTGAACAGTCACCATGTGTTCTTTCAAGATCTCTGTTACAAACCACTTTC	1681 CTGGTGGATAACAAAAGGTCTTTGGAACTCATCTCATGCAAGACATGGTGAAAGATGCA 1740 1741 CTTCGGTCTTTTGTCAGATCCTCCGAGTGCTTTCCCCCAAGTGCTACTATAAAATAC 1800 1741 CTTCGGTCTTTTGTCAGATCCTCCGAGTGCTTTCCCCCAAGTGCTACCTATAAAATAC 1800 1741 CTTCGGTCTTTTGTCAGATCCTCCGAGTGCTTTCCCCCAAGTGCTACCTATATAATAC 1800	1801 ACCAGGCTAAGGACTGTATCCACTCTTTGTTACTCACTGTGTTCGGCCATTCTGTAGTC 1860 1801 ACCAGGCTAAGGACTGTATCGACTCTTTGTTACTCACTGTTCGGCCATTCTGTAGTC 1860 1801 TATTCAGATCCATGGACATAACAGGCTCGACAGAGATAAGCTTGGTCATATTCTTG 1920 1861 TTATTCAGATCCATGGACATAACAGGGCTCGACAGAGATAAGCTTGGTCATATTCTTG 1920 1861 TTATTCAGATCCATGGACATAACAGGGCTCGACAGAGAGATAAGCTTGGTCATATTCTTG 1920	1921 AGGAATTIGCCACCTIGCAGGAIGAGTITAIGACATTITTATTITAATAGGCAGAGGAAGGT 1980
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JOURNAL Patent: WO 02064788-A 42 22-AUG-2002; Diadexus, Inc. (US) FEATURES Location/Qualifiers 1. 306 /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606" ORIGIN Query Match Query Match Doubles 3096; DB 6; Length 3096; Best Local Similarity 100.0%; Pred. No. 0; Matches 3096; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	8-8 E-E	121 CAAACCTCCAGGGTTTCCTTCGCCTTCGCCTTCTAAGAAATTCCCAGGGGCA	DD 181 GGGCAGACTCGGAGAGTCGGGGCTCCGGCCTCTTTCCGGGAACGCCCACTA 240 Qy 241 CCCAGGACTCCGACAGAGGTGAAAAAGATAACTTCCGGTCTCGGGATCGTCTCTAATC 300 [541 541 601		721 CTTTTGAAGCCATGTCTGCTATTGAAATGATGCACCAAGATGGATG	Db 781 GGAAACCAAGTIAATCGAAAAGTTCTCAATTTTGAACAAGCTATCAAGGATGGCACTATT 840

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SVWTPPPVHYLQFKEMSDINKYSPPPQSPELYVAASKHFQYTKMILENIPNPREVSR
ILKVAKPNEVYRKLLAGGHKKESKVPPFEDSSVHKYFPVVKLV"
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Mouse Embryonic Growth Associated Protein (EGAP)
Unpublished
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/product="embryonic growth-associated
/protein_id="AAMS2342.1"
/db_xref="G1:21539896"
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2, USA
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Pred. No. 0;
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Wenzlau,J.M. and Weiser-Evans,M.C.M.
Direct Submission
Submitted (13-MAY-2002) Pediatrics,
4200 East Ninth Ave, Denver, CO 8026
Location/Qualifiers
                                                                                                           organism="Mus musculus"
                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:10090"
/chromosome="11"
                                                                                                                                                         /dev_stage="embryo"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausher, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Mang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E.,
Bouterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Strausberg, R.
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Mus musculus RIKEN cDNA C030004C14 gene, mRNA (cDNA clone MGC:66717
INAGE:5707801), complete cds.
BC056435
BC056435.1 GI:33989782
MGC.
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                                                                                                                      1755 GAAAGTTCGTCCGTTGAGCCGAGAGATCACAATGAGCCAGGCCTATCAGAACATGTGTGC
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRRK plate: 124 Row: Kolumn: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21644570.
                                                                                                                                                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susama Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Danne Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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DEFINITION

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ELELYSWHEYYYIYWYLSEFLYAMLMSTLSRADGSQWAERINBEQQKGRSSKKTKKK
KKVRFLSREITMSQAYQUMCAGMFKTWVAFDMDGKVRFKFFLDSEQVRYEHRFAPFN
SVMTPPPVHYLQFRESSDLHKYSPPPQSPELYVAASKHFEQDAMILENIPPDREVGS
ILKVAKPNFVVWKLLAGGGHKKESKVPPEFDFSVHKYFPPVVKLV
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LGELLHDKLFGLFEAMSAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLSL
PELIGIMDTCFCCLITWLEGHSLAQIVFTCLYIHNPDFIEDPAMKAFALGILKICDIA
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N(alpha) terminal acetyltransferases contains MaklOp,
Maklip and Makly subunits. All three subunits are
associated with each other to form the active complex
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                                                                                                                                                                                                                                                                                                                    /note="Mak10; Region: Mak10 subunit, NatC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348; Indels
              /codon_start=1
/product="embryonic growth-associated"
/protein id="AAH56435.1"
/db_xref="GI:33989783"
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 1828.2;
ed. No. 0;
Mismatches
                                                                             xref="LocusID:78689"
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Pred.
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Matches 2154; C
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                                                                                                                                       2 (bases 1 to 2543)
Li,X. and Yu,F.
Direct Submission
Submitted (26-MAY-2000) The Schepens Bye Research,
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Codon start=1

product="corneal wound healing

protein id="AAF81791.1"

db_xref="GI:8926320"
                       is
                          gene
                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
Yi,X.J., Li,X.F. and Yu,F.S.
A novel epithelial wound-related gene
A noveloping rat cornea and skin
Curr. Eye Res. 20 (5), 430-440 (2000)
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58.1%; Score 1799.2;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 2139; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                  Street, Boston, MA 02114, USP
Location/Qualifiers
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Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACATCACCAGGCTCCACATCACG--GGAAGTGAGATGTGCTTTCTTGGGTAACAACTCAT
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                                                  GAAAGTTCGCCCATTGAGCCGAGAGATCACAATGAGCCAAGCATATCAGAACATGTGTGC
                                                                                          GAAAGTTCGTCCGTTGAGCCCGAGAGATCACAATGAGCCCAGGCCTATCAGAACATGTGTG
                                                                                                                                            TGGAATGTTTAAAACCATGGTAGCATTTGACATGGACGGCAAAGTACGTAAAACCGAAGTT
                                                                                                                                                                                                                                       TGAGCTTGATAGTGAACAAGTTCGGTATGAACACAGGTTTGCTCCATTCAACAGTGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF272892.1 GI:8926319
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GHILBEFATLQDEABKVDALHTMLKQEPQRQHLAMLGTWVLYHNLRIMIQYLLSGF
ELELYSPHRILLHILVSL"
                                                                                                                                                                                                                                                                     Submitted (19-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flodna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                        Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S. NEDO human cDNA sequencing project Unpublished
                                                                                                                                                                                                                                                                                                                                                            NEDO human cons. sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                            Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
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134. .1714
/note="unmamed protein product"
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Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center; Stanford University School of Medicine, Stanford, CA 94305

Meb site:

Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MONGSSVEEEGGGGGLGIPEKMRNNANWUDVTQEFKGACKELKL
GELLHUKLFGLFEAMSAIEMOPKNDAGMIGNVRKVLIPEDOAVKDEAIRVKDLSIP
ELIGIMDTCCCLITWLEGHSLAQTVPTCLYVHNPDLIQDPALKAFALGILKICDIAR
EKVNKAAVFEEEDFGAATYGFKOANNYTDLRVTGMLKUDVEDELQRKVKSTRSRGGGG
DPEVELDHQGCLALFSRVKFTRLLLSALISFTKKETSAVSEAQKLMSQAADLLPAVHA
ILGYGLGSQNDTYKGDHEJIMGFEBLYNDRALLPFPRYAAKITKRERWYNYFGSLIER
IKSVCEVINITNLASILDFFCEFSBGSPCVLSRSLLGTTFIJDNKKYPGTHAMQDMIK
DALRCFVSPPVLSSKCSLNNNHQAKDYIDSFVTHCTRPFCSLIQIHGHNRARQRDKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be found
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LELYSUHBYYYYYYYYYWYLSEFLYAWINGYTSRADSGWAEREN ILEBQLKYKSSKKGKYKK
KARPLSKETTINSQAYOMCAGWYKINIALDWDRKVBKPGFELDSGQWYYEHRAPPNS
VVTPPPVHYIQPKEMSDLKKYNPPPRSADLYMAASKHPQQAKLILLENVTSPDAEVNRI
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                                                                                                                                                          Direct Submission
Submitted (102-701-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 117 Row: n Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N(alpha)-terminal acetyltransferase. NatC
N(alpha)-terminal acetyltransferases contains Maklop,
Maklip and Maklp subunits. All three subunits associated with each other to form the active complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
               Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="Unknown (protein for MGC:64157)"
protein_id="AAH53286.1"
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Natc
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/note="Mak10; Region: Mak10 subunit,
                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="MGC:64157 IMAGE:6797204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="Kidney, zebrafish"
/clone_lib="NCI_CGAP_ZKid1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="Vector: pCMV-SPORT6.1"
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1. .2467
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                                                                                                                                    Strausberg, R.
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Matches 1648; Conserv
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Cypriniformes; Cyprinidae; Danio.

I (Dases 1 to 2467)

S Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Alschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Habh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant, T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
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1656 TIGAATIGGAACTCTACAGTATGCACGAGATACTATTACATATATGGTATCTCTCTGAA
                                                                                                                                                                                                                   ATTCAGATCCATGGACATAACAGGGCTCGACAGAGAGATAAGCTTGGTCATATTCTTGAG
                                                                                                                                                                                                                                                                            1439 ATTCAGATCCATGGACATAACAGGGCTCGACAGAGAGATAAGCTTGGTCATATTCTTGAG
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                                                                                              CAGGCTAAGGACTGTATCGACTCCTTTGTTACTCACTGTGTTCGGCCATTCTGTAGTCTT
                                                                                                                                       1379 CAGGCTAAAGAACTGTATCGACTCCTTTGTTACTCACTGTGTTCGGCCATTCTGTAGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1983 ATGCAGCGCTTCACACCATGCTGTTGAAACAGGAACCCCAAAGGCAACATTTGGCCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio
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ORGANISM
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DEFINITION
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RESULT 7

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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishi,S.,
Yamamo,Co,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                TTAAAACCATGGTAGCATTTGACATGGACGGCAAAGTACGTAAACCGAAGTTTGACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661 GGAGGTGGCCATAAAGGGGCAGAGTCTTCTTTCAGACCCAACTCTTAGAGGGCACATCAC
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      TTAAAACCATGGTAGCATTTGACATGGACGGCAAAGTACGTAAACCGAAGTTTGAGCTTG
                                                                                     ATAGTGAACAAGTTCGGTATGAACACAGGTTTGCTCCATTCAACAGTGTGATGACCCCGC
                                                                                                                 ATAGTGAACAAGTTCGGTATGAACACAGGTTTGCTCCATTCAACAGTGTGATGACCCCCCC
                                                                                                                                                                  CTCAGTCTCCTGAACTGTATGTGGCAGCTAGTAAGCACTTTTCAACAGGCAAAAATGATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       901 TACAGATTTAATCACAAATCATTTTTTATGAATGATTGAGTGAAAATAGTGTTTTATAAAG
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AKOS6059.1 GI:16551204
ACOS6059.1 GI:16551204
Homo sapiens (human)
Homo sapiens
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Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flodna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, S. - & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Ministry of Tokyo (partly supported by Science and Technology
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EHRFAPFNSVMTPPPVHYLQFKEMSDLNKYSPPQSPELYVAASKHFQQAKMILENIP
NPDHEVNRILKVAKPNFVVMKLLAGGHKKESKVPPEFDFSAHKYFPVVKLV"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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clone HSI07031.
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/clone_Tib="HSI"
/note="cloning vector pME18SFL3"
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Homo sapiens (human)
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/db_xref="GI:10439113"
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                                      Homo sapiens cDNA: FLJ22643 fis, AK026296
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/db_xref="taxon:9606"
/clone="HSI07031"
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                                                           Logari, T. Otsuki, T. and Sugiyama, T.

Slogai, T., Otsuki, T. and Sugiyama, T.

Direct Submission

Submitted (24-OCT-2011) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hti.co.jp, Tel:181-438-52-397; Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); CDNA ilbrary
CONSTRUCTION: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
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                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/mol_type="mkNA"
/db xzef="taxon:9606"
/clone="NT2NE2005317"
/cell_type="teratocarcinoma"
/cell_type="teratocarcinoma"
/clone_lib="NT2NE2"
/colone_lib="NT2NE2"
/note="cloning vector: pME18SFL3~mRNA from NT2 neuron after the differentiation of NT2 neuronal precursor cells."
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Pred. No. 7.2e-190;
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Oshima,A., Sugiyama,A., Kawakami,B.,
Nagahari,K., Masuho,Y., Nagai,K. and
NEDO human cDNA sequencing project
Unpublished
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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GACTTATGGATTTAAAATGGCTAACAGTGTGACAGATCTTCGAGTTACAGGCATGCTAAA
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/mol type="unassigned DNA"
/db xref="taxon:9606"
/noTe="Inoyte ID No: II:462889.1:2001JAN12"
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Patent: WO 02057304-A 7 25-JUL-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Sequence 7 from Patent WO02057304.
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Corby, N.
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                                                            73004 ATAATCAGCCAGGCCTATCAGAA-ATGTGGGCTGGAATGTTCAGAATGATGTTT
                                                                                        GACATGGACGGCAAAGTACGTAAACCGAAGTTTGAGCTTGATAGTGAACAAGTTCGGTAT
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Pred. No. 2.3e-139;
0; Mismatches 293;
                                  Mouse
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1. 84958
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85059. 87411
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Best Local Similarity 72.6%;
Matches 1105; Conservative 0
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Db 174940 GCGCAGACGGGCTCTGAGACTCCGGCTCTTTCCGGGAACCGCCCATA 174999 Qy 241 CCCAGGACTCCGACAGAGGTGAAAAACTTCCGGTCTCGCGATCGTCTCTAATC 300 Db 175000 CCCAGGACTCCGACAGAGGTGAAAAACTTCCGGTCTCGCGATCGTCTCTAATC 175059 Qy 301 TCGCGAGAAGAGAGCGCCCCATCGGCCGAACGGAGGCGGGGGGGTG 360 Db 175060 TCGCGAGAAGAGCGCCCCATCGGCCGAACGGAGGCGGGGGGGG	RESULT 13 AX778899 LOCAS LOCAS DEFINITION Sequence 1056 from Patent W003039443. ACCESSION AX778899 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX77889 VERSTON AX7788 VERSTON AX7788 VERSTON AX7788 VERSTON AX7788 VERSTON AX778 VERSTON AX778 VERSTON AX778 VERSTON AX778 VERSTON AX778 VERSTON AX778 VERSTON AX778 VE	Indwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten, PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE) FEATURES	Social Similarity 100.0%; Pred. No. 7e-89 se 440; Conservative 0; Mismatches 2548
Direct Submission JURNAL Submitted (08-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk COMMENT CAPERIS: clone-request@sanger.ac.uk During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSENCY; Tr:, TREMBL; Wp:, WORMPEP: Information on the WORMPEP Attabase can be found at http://www.sanger.ac.uk/Fbrojects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human Group. Further information can be found at http://www.sanger.ac.uk/enc/che/che/che/che/che/che/che/che/che/ch	FPI1-213G2 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAGe3.6 IMPORTANT: This sequence is not the entire insert of clone RP11-213G2 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-213G2 is at 181864 in this sequence. The true left end of clone RP11-65C15 is at 11320 in this sequence. The true right end of clone RP11-202111 is at 100 in this sequence. FEATURES Location/Qualifiers source //cnl.type="genomic DNA" //chromosome=""genomic DNA" //chromosome=""genomic DNA" //chromosome=""genomic DNA"	unsure //clone=lib="RPDI-213G2" unsure 39727	Query Match 17.8%; Score 551.4; DB 9; Length 181864; Best Local Similarity 99.8%; Pred. No. 9.4e-114; Dest Local Similarity 99.8%; Pred. No. 9.4e-114; Matches 552; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1 Trccrcacaaacrcccaaacrccraacarranacaaacraranacarranacacacac

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74372. 74537
/note="Single clone region. Assembly confirmed by
restriction digest data."
74706. 74920
/note="Single clone region. Assembly confirmed by
                     /note="Sequence from uni-directional dGTP big dye terminator reads only."
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Nucleic Acids Res. 30 (14), 3163-3170 (2002)
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Best Local Similarity
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Submitted (16-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Mar 21, 2002 this sequence version replaced gi:15787718.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr.: TREMBL; WD: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was many constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the stand content of constructed by the st
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RP11-37991 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                          300
                                                                                                                                                                              360
                                                                                                                                                                                                                                  AL161447 16-MAR-2003
Human DNA sequence from clone RP11-379P1 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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      CAGAGTCTTCTTTCAGACCCCAACTCTTAGAGGGCACATCACCAGGCTCCACATCACGGGA
                                       241 CAGAGTCTTCTTTCAGACCCAACTCTTAGAGGGCACATCACCAGGCTCCACATCACGGGA
                                                                                                                    2848 AGTGAGATGGATTTCTTGGGTAACAACTCATTATAAGGAATACTTTTAGTTTGACAGCCT
                                                                                                                                                                  301 AGTGAGATGGATTTCTTGGGTAACAACTCATTATAAGGAATACTTTTAGTTTGACAGCCT
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/organism="Homo sapiens
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/db_xref="taxon:9606"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 446)

Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,

Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Maravenko,O.V.,

Kisselev,J.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.

Not! flanking sequences: a tool for gene discovery and verification
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Homo sapiens genomic sequence surrounding NotI site, clone
NB6-015R.
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                                                                                                                                                                                                                                    /note="Tandem repeat. Forced join. Gap size estimated to
be approximately 300bp by restriction digest data."
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                                                                                                                     /note="Tandem repeat. Forced join. Gap size estimat
be approximately 200bp by restriction digest data."
129108
restriction digest data."

complement (74706. .74920)

/note="Sequence from uni-directional dGTP big dyeterminator reads only."
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2 (bases 1 to 446)
Zabarovsky.E.R.
Direct Submission
Submitted (16-WMY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
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                                                                                                        Location/Qualifiers
1. 446
/organism="Homo sapiens"
/organism="Homo sapiens"
/ol_type="genomic DNA"
/db xref="texon:9606"
/clone="NB6-015R"
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Search completed: August 11, 2004, 01:34:09 Job time : 12343.3 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August 10, 2004, 17:10:23; Search time 8425.09 Seconds (without alignments) 10973.574 Million cell updates/sec Run on:

Title:

1 ttcctcacgaaactcccagg......atttcttgacaaaaaaaa 3096 US-10-001-857-42 3096 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters: Searched:

55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database

gb_est1:*
gb_est2:*
gb_htc:*
gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:* em_esthum: *
em_estin: *
em_estwu: *
em_estpl: *
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em_estom:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ID		BC027201	AK021042	BM979022	BF969365
	DB	1	11	11	12	10
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	Score		795	777.8	705	8.969
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CB169246 VBB603020 AK050805 Mus muscu BG547889 602576187 R0465085 AGENOTION	_ =	928 646 827	AW00/583 WF02f11.X BUD58931 UI-M-FR0- BG112812 602285005 BC043701 Mus muscu BU613022 UI-M-FR0-	UI -M-GZO AGENCOUR' UI -M-GZO B0905B04 B0911G05	
CB169246 AK050805 BG547889 BO965085	514	925	AW007583 BU058931 BG112812 BC043701 BU613022	CF725470 BQ925670 CF725998 CF172281 CF172718	AAA888800 BC010475 BC710404 BC710475 BUS25571 CF9102089 ACR172581 ACR172581 CF916685 BUG57675 BC724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724711 CF724442 BM699453 BM699453 BM699453 CF916163
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ALIGNMENTS

BC027201 1033 bp mRNA linear HTC 19-NOV-2003 Mus musculus RIKEN cDNA C030004C14 gene, mRNA (cDNA clone IMAGE:4483189), containing frame-shift errors. Mus musculus (house mouse) BC027201.1 GI:20070883 RESULT 1 BC027201 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 [Dases 1 to 1033]

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Shemmen, C.M., Schuler, G.D., Alteschul, S.F., Zeeberg, B., Hentow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Mang, J., Hsieh, F., Stapleton, M., Soares, M.B., Bonaldo, M.F., Caaavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Cardinol, P., Panage, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Willalon, D.K., Mully, D.M., Sodergran, R.D., Fullyk, S.W., Villalon, D.K., Mull, Madan, A., Young, A., C., Rahe, S.S., Loquellano, D.K., Mull, Madan, A., Kodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Shevchenko, Y.,

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Mus musculus adult male corpus striatum cDNA, RIKEN full-lèngth enriched library, clone:C030004C14 product:CORNEAL WOUND HEALING RELATED PROTEIN homolog [Rattus norvegicus], full insert sequence.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
GGGAACCAAGTGAATAGAAAAGTTCTCAATTTTGAACAAGCTATCAAGGATGGCACCATT
                                     AAAATTAAAGATCTCACCTTGCCTGAACTGATAGGGATTATGGATACATGTTTTTGCTGT
                                                                 TIGATCACATGGCTCGAAGGCCATTCCTTGGCACAGACAGTGTTACGTGCCTTTACATT
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High-efficiency full-length CDNA
MECH. Enzymol. 303, 19-44 (1999)
9927923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortiun/LIML at: http://image.llnl.gov Series: IRAK Plate: 31 Row: i Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21644570 This clone has the following problem: frame shifted.

Location/Qualifiers
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   Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Bolckson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M., Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequence proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H.
                                                                                                                                                                                                                                   Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                       Mammalian
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/clonne="IRAGE:4483189"
/clonne="IRAGE:4483189"
/tissue type="Mammary tumor. Metallothionien-TGF alpha model. Io month old virgin mouse. Taken by biopsy."
/clone lib="NCT CGAP_Mam1"
/clone lib="NCT CGAP_Mam1"
/note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Pred. No. 3.3e-138;
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/mol_type="mRNA"
/strain="FVB/N"
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87.9%;
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komo,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 973)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Aratun, H., Hara, A., Hayatsu, N., Hiramoto, K., Hiranoto, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Satto, H., Satto, R., Sakai, C., Sakai, K., Sano, H., Sagaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Team and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RIKEN Genome Exploration Research Group Phase II
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:C030004C14"
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COMMENT

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/tissue_type="corpus striatum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489 ATTIGGTACATIGCACGGGAAAAAAAAAAAAAGCTGCTGTTTTCGAAGAAGAATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549 CAGICAAIGACATACGGATITAAAAIGGCCAACAGTGTGACAGATTTCCGAGTTACAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CORNEAL WOUND HEALING RELATED PROTEIN homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [Rattus norvegicus] (SPTR|Q9JI01, evidence: FASTY, 96.2%ID, 43.5%length, match=948) putative"
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0
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Pred. No. 5.4e-135;
0; Mismatches 117; Indels
xref="taxon:10090"
/db_xref="taxon:1000
/clone="C030004C14"
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848

FEATURES

2439

664

7

2499

604

2559

544

2619

484

2679

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424

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ATGCATTGATGAACGTTATATGGTTTTATTACAGATTTAATCACAAATCATTTTATGA 3039
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602271630F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4359702 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 TICTIGGGIAACAACTCATTATAAGGAATACTITTAGTTIGACAGCCTTATATGACATGA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ATGAAAACTGCTGTTTTAAAGTGGTTTATTATGTTCCATGGAAGAAACTGGTCTTATTGA 124
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 TAATAGAATTTTAAAAGGTTGCCAAACCCAACTTTGTGGTTATGAAGTTATTGGCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 ACACAAAAAGGAATCTAAAGTTCCTCCTCGAATTTGATTTCTCTCCTGCTCATAAATATTTTCC
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                                                                                                                                                                                                           2380 CAAAGTACGTAAACCGAAGTTTGAGCTTGATAGTGAACAAGTTCGGTATGAACACAGGTT
                                                                                                                                                                                                                                           2440 TGCTCCATTCAACAGTGTGATGACCCCGCCGGCGGTGCACTACTTACAGTTCAAGGAAAT
                                                                                                                                                                                                                                                                                                                                       GTCTGACCTCAATAAATATAGCCCTCCTCCTCAGTCTCCTGAACTGTATGTGGCCAGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 603 GTCTGACCTCAATAAATATAGCCCTCCTCCTCAGTCTCTGAACTGTATGTGGCAGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAGCACTTTCAACAGGCAAAAATGATATTGGAAAATATTCCTAACCCGGACCATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 TAAGCACTITCAACAGGAAAAATGATATTGGAAAATATTCCTAACCCGGACCATGAGGT
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TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-DUI
TAG_SEQ=GGCTGTAGGC"
                                                                                                                                                                    1;
                                                                                                                 Length 722;
                                                                                                                                                                  Indels
                                                                                                                                                                  .,
                                                                                                                    Score 705; DB 12;
Pred. No. 2.2e-121;
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF969365.1 GI:12336580
                                                                                                                      22.8%;
99.9%;
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Homo sapiens
                                                                                                                                                                  Matches 716; Conservative
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Best Local &
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BF969365
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/ dev stage="Adult"
/ dev stage="Adult"
/ dev stage="Adult"
/ dev stage="Adult"
/ dev stage="Adult"
/ dev stage="Adult"
/ dev stage="Adult"
/ done lib="Ulu"
/ done lib="Ulu"
/ done lib="Ulu"
/ done lib="Ulu"
/ done lib="Ulu"
/ done lib="Ulu"
/ done lib="Ulu"
/ done lib="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site=l: EocR !; Site=l: Not !;
/ Ul-CF-DUI is a normalized cDNA lib=xxy containing the following tissue(s): Primary Lung Epithelial Cells The lib="Ary was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (AT) B tail. The sequence tag for this
                                                                                                                         1500
                                                                                                                                                                                                                                                                                                                                                   UI-CF-DUI-adl-c-13-0-UI.sl UI-CF-DUI Homo sapiens cDNA clone
UI-CF-DUI-adl-c-13-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: paul mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Expending by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. L (bases 1 to 722)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                          849 CACACCTCATTGCACCACGGCATCCAGGCTCAGAATGGCACTACCAAAGGAGACCATCCA
                               1381 CATAATTCATTGCATCATGGCATCCAGGCCCCAGAATGATACTACAAAAGGAGATCATCCA
                                                                                                                           University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="UI-CF-DU1-adl-c-13-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery
Genome Res. 6 (9), 791-806 (1996)
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library is GGCTGTAGGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (www.openbiosystems.com).
Seg primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
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BM979022/c
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AUTHORS
TITLE
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PUBMED
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KEYWORDS
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2859

244

2919

2979

3019

778

720

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CB169246 814 bp mRNA linear EST 30-JAN-2003
VBB603020215.R1 CSEQFXN41 testes Bos taurus cDNA, mRNA sequence.
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    --TCCCAATCATTTTTATGAATGATTG-GTGCACATCGGTTTTAACGTGATAAATTCTTG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814 AIGGITCAAGCAGCAGAICTITTCIGCCATICATAATICATIGCAICAIGGIAICCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol trye="mana"
//db xref="taxon:9913"
/tissue trye="testes"
/tissue trye="testes"
/clone lia="CSBQFXN41 testes"
/note="Organ: testes; Vector: pBluescript SK+; Site_1:
/note="Organ: testes; Vector: pBluescript SK+; Site_1:
/note="Organ: testes; Vector: pBluescript SK+; Site_1:
/clone lia Site_2: EcoRI; sequence 5' of the insert
/s'-NNN. _NNNINSERS
/clone lia serts (ArganTCGATATCGATATCGATACGATGCACCTCGAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             normalized Rd 1 library, sequenced 3' with M13R primer.
                                                              2903 AGCCTTATATGACA-TGAAAACTGCTGTTTTAA-AGTGGTTTATTATGTTCCAT-G
                                                                                                  AGCCTTATATGACATGAAAACTGCTGTTTTAACAGTGGTTCTTTATGTTCCCTGG
                                                                                                                                                                  2960 GAAGAAACTGGTCTTATTGAATGCATTGATGAACGTTATATGGTTTTATTACAGATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1348 ATGGTTCAAGCAGCAGAATCTTCTTCTGCCATTCATAATTCATTGCATCATGGCATCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  754 GCCCAGAATGACACTAACAAAAGGAGACCATCCCATTATGATGGGTTTTGAGCCACTTGT
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90.3%; Pred. No. le-112;
Nigmatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .814
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Bovine ESTs (Adelson and G
Unpublished (2003)
                                                                                                                                                                                                                                                                                               3080 TCTTGACAAAAAAA 3095
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CB169246.1 GI:28155372
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CB169246/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                             /tissue_type="adrenal cortex carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NNH MGC 84"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
Not1; Site_2: Sall; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM9999 row: 1 column: 07
High quality sequence stop: 785.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2784 GGGGCAGAGTCTTCTTTCAGACCCCAACTCTTAGAGGGCACATCACCAGGCTCCACATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATCACAATGAGCCAAGCATATCAGAACATGTGTGCTGGAATGTTTAAAAACCATGGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 696.8; DB 10;
Pred. No. 7.5e-120;
0; Mismatches 37;
                                                                                                                                                                                                                                                  1. .854
/organism="Homo sapiens"
                      Ph.D.
                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4359702"
                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                  Contact: Robert Strausberg, F
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.5%;
Best Local Similarity 94.5%;
Matches 809; Conservative
  Unpublished (1999)
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L. Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Golome Exploration Research Group, RIKEN Golome Exploration Research Group, RIKEN Golome Conter (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-reseges-riken.go.jp, Texas. 141-45-503-9222, Pax. Bl. 145-503-9216)
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,Y., Ishi,Y., Nakamira,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yongaza,Y., Ishikawai,T., Ozawa,Y., Tamaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/61"
/db_xref="FANTOM DB:D030020M24"
/db_xref="Texton:10090"
/db_xref="texton:10090"
/clone="no30020M24"
/tissue_type="whole body"
/clone_lb="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3071)
                                                                                                                                                                                                                                                                                                                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research
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1. 3071
/note="CORNEAL WOUND HEALING RELATED PROTEIN homolog
[Rattus norvegious] (SPTR|Q9J101, evidence: FASTY,
96.2%ID, 43.5%length, match=948)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Mus musculus 9 days embryo whole body cDNA, RIKEN Full-length
enriched library, clone:D030020M24 product:CORNEAL WOUND HEALING
RELATED PROTEIN homolog [Rattus norvegicus], full insert sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Contact: Robert Strausberg, Ph.D.
Email: Captbernent: CLOWTECH Laboratories, Inc.
Tissue Procurement: CLOWTECH Laboratories, Inc.
CDNA Library Preparation: CLOWTECH Laboratories, Inc.
CDNA Library Preparation: CLOWTECH Laboratories, Inc.
CDNA Library Preparation: CLOWTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://mage.llh.gov.n. column: 21
High quality sequence stop: 738.

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Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.

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Homo sapiens (human)

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IMAGE:2064845 3' similar to WP:T23B12.4 CE14032 ;, mRNA sequence.
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CITITIGAAGCCATGICTGCTATTGAAATGATGGATCCTAAGATGGATGCCGGTATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 CATAATCCCGACTICATAGAAGATCCTGCCATGAAAGCTTTTGCTCTGGGAATCTTGAAG
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                                                                                                                               GGAAACCAAGTTAATCGAAAAGTTCTCAATTTTGAACAAGCTATCAAGGATGGCACTATT
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Other ESTs: u102b03.y1
Other ESTs: u102b03.y1
Contact: Marra M/Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
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IMAGE: 6509503 5', mRNA sequence.
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/tissue type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone lib="NH1 MGC 134"
/note="Vector: pGWV-SPORT6 1; Site 1: BcoRV; Site 2: NotI;
cloned undirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                          541 AGGAATCTAAAGTTCCTCCTGAATTTGATTTCTCTGCTCATAAATATTTTCCTGTAGTGA
                                                                                                                                                                                                                        2748 AACTTGTTTGAGAGAGTTGGGGGAGGTGGCCAT-AAAGGGGCAGAGTCTTTCAGACC
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                                                       2688 AGGAATCTAAAGTTCCTCCTGAATTTGATTTCTCTGCTCATAAATATTTTCCTGTTGTGA
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can lette://image.llni.gov

Plate://image.llni.gov

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Column: 08
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0; Mismatches 100; Indels
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/mol_type="mRNA"
/db xref="taxon:10090"
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Location/Qualifiers
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Mus musculus
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/db xref="Laxon:10090"
/clone="IMAGE:30540139"
/tissue type="whole eye"
/dev stage="whole eye"
/dev stage="whole eye"
/dev stage="mbxpo 15.5,16.5,17.5,18.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP GW0"
/note="Organ: Eye; Vector: pXx- Ast; Site 1: EcoR I;
Site 2: Not 1; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel:First strand cDNA synthesis was primed with Oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor digested with NotI and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CTGCGTCCTC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                    CATCATGGCATCCAGGCCCAGAATGATACTACAAAAGGAGATCATCCAATTATGATGGGT 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD808079 786 bp mRNA linear EST 15-JUL-2003 UI-M-GW0-ciq-n-20-0UI.rl NIH BMAP_GW0 Mus musculus cDNA clone IMAGE:30540139 5', mRNA sequence.
                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This, clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                   GAAGCTCAAAAATTGATGGTTCAAGCAGCAGATCTTCTTCTGCCATTCATAATTCATTG
             CACCACGCCATCAAGGCTCCGAATGGCACTACCAAAGGAGACCATCCAATTAAAATGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 786)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                TITGAACCCCITGIGAACCAGAGGCTACTICCACCTACCTICCCICGAI 1501
                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  program coordinator."
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Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6"
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CD808079.1 GI:32466905
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Eukaryota, Metazoa, C
Mammalia, Eutheria, R
1 (bases 1 to 786)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: pYX-5.
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                                                                                                                                                                                                                                                                                                                                     /clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney mkia"
/mote="Organ: kidney; Vector: pWE185-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGCCTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pWE185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCACCTTGCCTGAACTGATAGGGATTATGGATACATGTTTTTGCTGTTTGATAACGTGG 912
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Possible reversed clone: similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 509.
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                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                          /clone="IMAGE:2064845"
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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/mol type="mRNA"
// db xref="mRNA"
// db xref="mRNA"
// db xref="mRNA"
// done="UI-CF-DUI-adr-h-18-0.UI"
// tissue type="Primary Lung Epithelial Cells"
// dev stage="Adult"
// dev stage="Adult"
// dev stage="Dil" dev colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for colling for this site and the (dI) sequence that is located between the Not I is colling for this
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                                                                                                                                                                                                                                                                                    Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
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1 (bases 1 to 616)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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TAG TISSUB-Lung Bpthelial Cells Tissue nos 359-368
TAG_LIB-UI-CF-DUI
TAG_SEQ-GGCTGTAGGC"
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                                                                                                                                                                                     University of Iowa 2024 University of Iowa Med Labs, Iowa City, Tel: 319 356 4866
Fax: 319 356 7171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Homo sapiens"
                                                                                        Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
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Seg primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                         Contact: McCray, PB
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Matches 610; Conservative
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PUBMED
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                                                                                             1150 GATGTGGAGGATGACATGCAAAGAAGAGTAAAGAGTACTCGAAGTCGACAAGGAGAAGAA 1209
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                      61
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                                                                                                                                    1210 AGAGATCCAGAAGTTGAACTAGAACACCAACAATGTTTAGCAGTATTCAGCAGAGTGAAA
                                                                                                                                                                                                                                                                         GTCTGTGAGGTTGTGAATTTAACAAATTTACATTGTATCCTGGATTTTTTTCTGTGAATTT
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                                                5;
    DB 14; Length 786;
                                              Indels
                       Pred. No. 1.2e-108;
0; Mismatches 87;
      Score 636.8;
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  Query Match 20.6%;
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BM979511/c
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with EcoR I adaptor , digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Inva Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111 AACAGTGTGACAGATCTTCGAGTTACAGGCATGCTAAAAGATGTGGAGGATGACATGCAA 1170
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                                                                                                                                                                                                                                                                                         GGAGAACTACTTCATGATAAGCTATTTGGTCTTTTTGAAGCCATGTCTGCTATTGAAATG
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                                                                                                                                                                                                           Length 721;
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AGENCOURT 11295472 NIH MGC 164 Mus musculus cDNA clone IMAGE:30146905 5', mRNA sequence.
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                     Score 602.6; DB 14;
Pred. No. 3e-102;
0; Mismatches 74; I
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CA977646.1 GI:27510300
                                                                                                                                                                                                     Query Match 19.5%;
Best Local Similarity 89.7%;
Matches 647; Conservative
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/db_xref= taxon:10090"
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/tissue_type="Upper Head"
/dev stage="9.5 and 10.5 dpc"
/lab_nost="DH10B (T1 phage resistant)"
/lab_nost="DH10B (T1 phage resistant)"
/clone lib="NTH BMAP HJ0"
/clone lib="NTH BMAP HJ0"
/clone lib="NTH BMAP HJ0"
/site_2: Not I; The library was constructed according Bonaldo, Lemnon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarcse gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site Double strand cDNA was size fraction, iligated
                                                              GCAGAGTCTTCTTTCAGACCCCAACTCTTAGAGGGCACATCACCAGGCTCCACATCACGGG 2846
                                                                                                                                                AAGTGAGATGGATTTCTTGGGTAACAACTCATTATAAGGAATACTTTTAGTTTGACAGCC 2906
                                                                                                                                                                                                                                    TTATATGACATGAAAGAAACTGCTGTTTAAAGTGGTTTATTATGTTCCATGGAAGAAA 2966
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                                                                                                   GCAGAGTCTTTTTTTCAGACCCAACTCTTAGAGGGCACATCACCAGGCTCCACATCACGGG 257
Angreachideaririceridegerancharcheriarangeariacriringringachece 197
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Email: cgapbs.rémail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                              CIGGICTIATIGAAIGCATIGAIGAACGITATAIGGITTIATIACAGAITTAAICACAAA 77
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 721)
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UI-M-HJO-cmi-l-06-0-UI.rl NIH BMAP_HJO Mus musculus cDNA clone
IMAGE:30626477 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (house mouse)
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/_clone_lib="NITH MGC_96"
/_clone_lib="NITH MGC_96"
/_clone="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamH1; Site_2: SalI-XhoI (gtoga); Oligo-dT primed using primer size 2:3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI602827 697 bp mRNA linear EST 07-SEP-2001 603247187F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5294804 5',
---AGGCAGAGAAGGTTGATGCAGCGCTTCATACTATGTTGTTGAAACAG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 697)
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tobhiyuki and Piero Carninoi (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                 698 AGCCGCCAAAAACCAAGAAAAAAAAAAAGTTCGTCCGTTGAGCCGAGAGTTCAATG
                                                                        2015 GAACCCCAAAGGCAACATTTGGCCTGTTTAGGTACCTGGGTCCTTTACCATAACCTTCGC
                                                                                                                                         GAGCCTCAGAGACAACATCTGGCCTGCTTAGGAACCTGGGTTCTTTACCATAACCTCCGG
                                                                                                                                                                                                              2075 ATTATGATACAGTACCTTCTAAGTGGCTTTGAATTGGAACTCTACAGTATGCACGAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2255 AGTAGTAAAAAAAAAAAAAAAAAAAAAAAAGAAAGTTCGCCCATTGAGCCGAGAGATCAAATG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
Plate: LLAM11745 row: n column: 21
High quality sequence stop: 643.
Location/Qualifiers
1. .697
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/clone="IMAGE:5294804"
/tissue_type="hypothalamus"
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BI602827.1 GI:15495766
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/lab host="DH10B (phage-resistant")"
/clone=lib="UHH MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_164" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" | MGC_165" 
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                                                                                                                   Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                        Contact: Nobert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Gappbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAMO063 row: f column: 02
High quality sequence stop: 655.
Location/Qualifiers
rce
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                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
J. (bases 1 to 900)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol_type="mRNA"
/db xref="taxon:10090"
                                                      Mus musculus (house mouse)
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organism="Homo sapiens"
                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2506317"
/sex="pooled"
                                                                                                                                                                                                                                                                                                                                                                                  normalization.
                                                                                                                                               1. .598
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                                                                                                                                                                                                                                                                                                                                                 546 TTTTGCTCTGGGAATCTTGAAATCTGTGACATTGCAAGGGAAAAAGTACAATAAAGCTG
                                                                                                                                                        CGTGGCGGCGCGGGTGACCACGGGAGGAGGTAGGCATAATGGTAATGAAAGCTTCTGTAGA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
                                                                        1;
                                             Length 697;
                                                                        Indels
                                             12;
                                                                                                 GAGAGGGGGGGGGCGCCGGCCGAGGCGCCGTCGTTAI
                                        Score 598.8; DB 12
Pred. No. 1.5e-101;
0; Mismatches 2;
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NIH MGC Library."
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ilarity 99.5%;
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cDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 115 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 459.

High quality sequence stop: 459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="colon"
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/clone_lib="NGI_CGAP_CO3"
/clone_lib="WGI_CGAP_CO3"
/note="Vector: pT713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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19.3%; Score 597; DB 9; I
Best Local Similarity 99.8%; Pred. No. 3.4e-101;
Matches 597; Conservative 0; Mismatches 1;
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Search completed: August 11, 2004, 04:18:40 Job time: 8430.09 secs

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GenCore version 5.1.6
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using sw model - nucleic search, OM nucleic

(without alignments) 10594.393 Million cell updates/sec August 10, 2004, 17:10:17 ; Search time 1241.45 Seconds Run on:

US-10-001-857-42 3096 Title: Perfect score:

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IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues

6747726 Total number of hits satisfying chosen parameters:

length: 0 length: 200000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:*
geneseqn2002s:*
geneseqn2003as:*
geneseqn2003bs:* N_Geneseq_29Jan04:* qeneseqn2003cs:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

Description	Abq75303	Adc30041 Human	Abv29823 Human	Abv23940 Human			_		Adc31969 Human nov								_	_	Abl07143 Drosophi	Abq75302 Human lun	_	Abl07142 Drosophi	
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ALIGNMENTS

Human, lung, lung specific nucleic acid; LSNA; lung specific protein; LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer; squamous cell carcinoma; gene; chromosome 9; ss. Human lung specific nucleic acid sequence SEQ ID NO:42. ິວ Liu Sun Y, BP. Chen S, ABQ75303 standard; cDNA; 3096 20-NOV-2000; 2000US-0252054P. 20-NOV-2001; 2001WO-US045080. (first entry) Macina RA, Recipon H, (DIAD-) DIADEXUS INC. WO200264788-A2. 05-NOV-2002 22-AUG-2002. ABQ75303; Ношо RESULT 1 ABQ75303

WPI; 2002-657601/70.

New lung specific nucleic acid useful in gene therapy or as vaccines for treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous lung diseases, as well as for diagnosing, monitoring or staging these diseases.

Claim 1; Page 168-169; 282pp; English.

The present invention describes an isolated lung specific nucleic acid (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid sequences comprising 17 - 73 amino acids, given in ABB52873 to ABP52865; (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b), or (d) has 60 % sequences identity to (a) or (b). LSNA and lung specific protein (LSP) sequences have cytostatic activity and can be used in gene therapy and vaccines. LSNAs and LSPs are useful for diagnosing and monitoring the presence and metastases of lung cancer in a patient. An

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antibody that specifically binds to an LSP can be used for determining the presence of an LSP in a sample, as well as for treating a patient with lung cancer, particularly by inducing an immune response against the lung cancer cell expressing the LSNAs or LSPB. In particular, these LSNAs and LSPB are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer (e.g. squamous cell carcinoma) and noncancerous disease states in lung
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ADC30041 ID ADC RESULT

CDNA; 3029 standard; ADC30041

ADC30041;

(first entry) 18-DEC-2003

Human novel cDNA sequence, SEQ ID NO:123.

antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; gene therapy; chromosome 9; gene; ss.

Homo sapiens.

WO2003029271-A2

10-APR-2003

24-SEP-2002; 2002WO-US030474.

24-SEP-2001; 2001US-0324631P.

(HYSE-) HYSEQ INC.

., H Wehrman Weng ٦, Wang J, Wang Z, v, v , Zhao (Asundi ΑJ, Wang D, Ma Y, Drmanac RT; Zhang J, Ghosh M, Haley-Vicente D, rang TY,

2003-371981/35. WPI;

P-PSDB; ADC31012

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

Claim 1; SEQ ID NO 123; 1185pp; English.

The invention relates to 971 novel human cDNA sequences (ADC29919-ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of polymucleotides or polypeptides of the invention; and methods of invention further discloses methods to perventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC32628) and the polypeptides encoded by the contigs (ADC32628 ADC3384). The nucleic acids and polypeptides of the invention are useful in diagnostics drug screening forms. useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, placiet diseases, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

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cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2608 GGCGGCGTCGTTATTTCCGTGGTCCGGACAGTGCGTGGCGGCGCGCGGGTGACCACGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                               Human prostate expression marker cDNA 29814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2577.8;
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0; Mismatches
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BP.
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98.8%;
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Matches 2638; Conservative
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TTCATTGCATCATGCCATCCAGGCCCCAGAATGATACTACAAAAGGAGATCATCCAATTAT 1445
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                                                                                                                                                                                CGCATGCGTGCACGCTGCCGGTCGGGCTGGGCTGAGAGGGGAAGGGGGCGGCGGCGGCGGCCGA
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                                                                                       Score 2577.8;
Pred. No. 0;
a pharmacodyanamic
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98.8%;
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is also useful
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Matches 2638; Conserv
                                            Sequence 2668
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                                                                 234
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                  TCACCAGGCTCCACATCACGGGAAGTGAGATGGATTTCTTGGGTAACAACTCATTATAAG
                                                                                                                                      GAATACTITITAGITITGACAGCCTTATATGACATGAATGAAAACTGCTGTTTTAAAGTGGT
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                                                          TCACCAGGCTCCACATCACGGGAAGTGAGATGGATTTCTTGGGTAACAACTCATTATAAG
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2000US-0189862P.
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pharmacogenomic
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Human; molecule for disease detection and treatment; MDDT; gene therapy; cytostatic; antiatretriosclerotic; hepatotropic; anti-HIV; antiallergic; antiinflammetory; antiasthmatic; cerebroprotective, nootropic; neuroprotective; antiparkinsonian; cardiant; antianginal; gene; ss.
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                                                 CCTCCTCAGTCTCCTGAACTGTATGTGGCAGCTAGTAAGCACTTTCAACAGGCAAAAATG
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The present invention relates to human proteins and coding sequences of molecules for disease detection and treatment MDDT. The sequences can be used in the treatment of diseases associated with the decreased expression or overexpression of MDDT, such as cell proliferative (cancer, atherosclerosis, hepatitis), autoimmune/inflammatory (e.g. AIDS, atlergaes, asthma), developmental (dwarfism, renal tubular acidosis), neurological (e.g. stroke, Parkinson's disease, epilepsy) and cardiovascular (congestive heart failure, myocardial infarction, angina pectoris) disorders. The present sequence is a coding New human molecules for disease detection and treatment (MDDT), useful for diagnosing, treating and preventing diseases or conditions associat with the aberrant MDDT expression, e.g. cancer, AIDS, asthma, diabetes, Baughn MR, Yao MG, Walia NK, Elliot VS, Xu Y;
CD, Yue H, Ding L, Gietzen KJ, Ison CH, Lu DAM;
AJA, Ghandi AR, Thangavelu K, Sanjanwala MM, Tang YT;
J, Griffin JA, Swarnaker A, Azimzai Y, Sapperstein S
N, Lee EA, Lu Y, Tran UK, Marquis JP; infarction, angina pectoris) disorders. sequence of the invention Claim 11; Page 159-160; 177pp; English. GENOMICS WPI; 2002-713453/77 P-PSDB; AAO19400. INCYTE Honchell CD, Hafalia AJA, Burford N, hepatitis.

T; 0 U; 0 Other; Sequence 2488 BP; 768 A; 461 C; 567 G; 692

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1613 1493 1193 1253 1313 1373 1433 1853 1378 1973 2033 1535 2093 1595 2153 CTTGAAAATCTGTGACATTGCAAGGGAAAAGTAAATAAAGCTGCTGTTTTTGAAGAGGA AGATTTTCAGTCAATGACTTATGGATTTAAAATGGCTAACAGTGTGACAGATCTTCGAGT TACAGGCATGCTAAAAGATGTGGAGGATGACATGCAAAGAAGAGTAAAGAGTACTCGAAG TACAGGCATGCTAAAAGATGTGGAGGATGACATGCAAAGAAGAGAAGATAAAAGACTACTCGAAG TCGACAAGGAGAAGAAGGATCCAGAAGTTGAACTAGAACACCAACAATGTTTAGCAGT TCGACAAGGAGAAGAAGAAGTCCAGAAGTTGAACTAGAACACCAACAATGTTTAGCAGT ATTCAGCAGAGTGAAATTTACTCGTGTGTTACTGACAGTGCTTATAGCCTTTACTAGAA ATTCAGCAGAGTGAAATTTACTCGTGTGTTACTGACAGTGCTTATAGCCTTTACTAAGAA AGAGACCAGTGCTGCTGCAGAAGCTCAAAATTGATGGTTCAAGCAGCAGCAGTCTTCTTTC TGCCATTCATAATTCATTGCATCGTGCCATCCAGGCCCAGAATGATACTACAAAAGGAGA TGCCATTCATAATTCATTGCATCATGGCATCCAGGCCCCAGAATGATACTACAAAAGGAGA TCATCCAATTATGATGGGTTTTGAACCCCTTGTGAACCAGAGGCTACTTCCACCTT CCCTCGATATGCAAAATAATTAAAAGGGAAGAAATGGTGAACTATTTGCAAGATTAAT CCCTCGATATGCAAAATAATTAAAAGGGAAGAAATGGTGAACTATTTTGCAAGATTAAT AGATAGAATAAAAACTGTCTGTGAGGTTGTGAATTTAACAAATTTACATTGTATCCTGGA TrititicigidaAtritAGIGAACAGICACCAIGIGITICITICAAGAICTCIGITACAAAC AGATGCACTTCGGTCTTTTGTCAGATCCTCCGAGTGCTTTCCCCCCAAGTGCTACTATAT AGATGCACTTCGGTCTTTTGTCAGTCCTCCG--GTGCTTTCCCCCAAGTGCTACCTATAT <u> AATAATCACCAGGCTAAGGACTGTATCGACTCCTTTGTTACTCACTGTGTTCGGCCATTC</u> TGTAGTCTTATTCAGATCCATGGACATAACAGGGCTCGACAGAGAGATAAGCTTGGTCAT TGTAGTCTTATTCAGATCCATGGACATAACAGGGCTCGACAGAGAGATAAGCTTGGTCAT ATTCTTGAGGAATTTGCCACCTTGCAGGATGAGTTTATGACATTTTAATTAGGCAG -----AGGCAG AGAAGGTTGATGCAGCGCTTCACACCATGCTGTTGAAACAGGAACCCCAAAAGGCAACATT TAAGTGGCTTTGAATTGGAACTCTACAGTATGCACGAGTACTATTACATATTGGTATC <u> AATAATCACCAGGCTAAGGACTGTATCGACTCCTTTGTTACTCACTGTGTTCGGCCCATTC</u> TGGCCTGTTTAGGTACCTGGGTCCTTTACCATAACCTTCGCATTATGATACAGTACCTTC AGAAGGTTGATGCAGCGCTTCACACCATGCTGTTGAAACAGGAACCCCAAAGGCAACATT ATTCTTGAGGAATTTGCCACCTTGCAGGATG 1134 1194 1254 1314 841 1434 1494 1021 1554 1081 1614 1141 1674 1201 1734 1261 1319 1854 1379 1914 1439 1974 1476 2034 601 199 721 781 901 196 2094 à Ωp ð qq à qq ò q ð qq 8 Ω 8 g ð g Š ద ð 셤 à g à 원 Š g ₹ 셤 Š g 8 g ð g à

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                                                                                                                                                                                                                                                                                                                                                                                                                                 2196 CTAAAGTTCCTCCTGAATTTGATTTCTCTGCTCATAAATATTTTCCTGTTGTGAAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGAGAGAGACTGGGGAGGTGCCATAAAGGGGCAGAGTCTTCTTTTCAGACCCAACTCT
                     TCTCTGAATTCCTTTACGCATGGTTGATGTCAACATTGAGTCGTGCCGATGGCTCTCAAA
                                                               TGGCAGAGGAAAGGATAATGGAAGAGCAGCAGAAAGGCCGTAGTAGTAAAAAACAAAGA
                                                                                                        AAAAAAAGAAGTTCGCCCATTGAGCCGAGAGATCACAATGAGCCAAGCATATCAGAACA
                                                                                                                                                                                                                                     GIGIGATGACCCCCCCCCCCAGTGCACTACTTACAGTTCAAGGAAATGTCTGACCTCAATA
                                                                                                                                                                                                                                                                                AATATAGCCCTCCTCCTCAGTCTCCTGAACTGTATGTGGCAGCTAGTAAGCACTTTCAAC
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Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox

Claim 44; SEQ ID NO 4174; 874pp; English.

mean values.

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Orr

Castle A,

Higgs B,

Johnson K,

Porter M,

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Mendrick I Elashoff N

WPI; 2003-731472/69.

(GENE-) GENE LOGIC INC

2002US-0378652P 2002US-0378653P 2002US-0394230P 2002US-0394230P 2002US-0394253P 2002US-0407688P

09-JUL-2002; 04-SEP-2002;

2002US-0353171P. 2002US-0363534P. 2002US-0370248P. 2002US-0371134P. 2002US-0371135P. 2002US-0371150P. 2002US-0371150P.

10-APR-2002; 10-APR-2002;

2003WO-US003482

04-FEB-2003;

Rattus norvegicus WO2003065993-A2. 2002US-0373602P. 2002US-0374139P. 2002US-0378370P

10-APR-2002; 2 11-APR-2002; 2 19-APR-2002; 2 22-APR-2002; 2 22-APR-2002; 2 09-MAY-2002; 2 09-MAY-2002; 2 09-MAY-2002; 2

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The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCATAATGGTTATGAAAGCCGCAGTAGATGATGACGCTTCGGGATGGGAGCTCAATGTC 117
                                                                                                                                                                                                                                                                                                                                                                          may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCATAATGGTTATGAAAGCTTCTGTAGATGATGACGATTCAGGATGGGAGCTCAGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.1%; Score 1799.2; DB 9; 84.0%; Pred. No. 0; ive 0; Mismatches 343; ]
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Conservative
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Matches 2139; Conserv
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diagnostic marker;

hepatocyte toxicity modelling related gene SEQ ID NO:4174

BP

ADB53632 standard; DNA; 2543

RESULT 6 ADB53632

ADB53632;

(first entry)

Primary rat 04-DEC-2003

toxic effect; gene expression profile; hepatotoxicity; toxicity marker, toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.

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2458
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                                                                                                                                         TATTACAGACTTCATTGTAAAACTTTTTTAATGAATGATTGTGTG-AAATAGTGTTTGTA
                2344 TICAGIAICAGIACAACACCCITACCIGGAGAGGAACG-AAACIGCIGITITAAAGIGGIT
                                                  TATTATGTTCCATGGAGAAAACTGGTCTTATTGAATGCATTGATGATGATGTTATATGGTTT
                                                                                 TGTTATACTCCATGGGTGTGTGACGGG----CTGGAATGCATTGGTGAACGTTACATGGTTT
                                                                                                                 TATTACAGATTTAATCACAAATCATTTTTATGAATGATTGAGTGAAAATAGTGTTTATA
 Jones
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V, Daffo A, Marwaha R,
David MH, Lewis SA;
                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding human secretory protein #7.
                                                                                                                                                                            AAGGITAATAAATTTCTTGACAAAA 3091
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Dam TC, Liu TF, Harris B, Flores
Chang SC, Gerstin EH, Peralta CH,
                                                                                                                                                                                                AAGGTTAATAAATTTCTTGACAAAA
16-JAN-2001; 2001US-0261864P.

16-JAN-2001; 2001US-0261865P.

16-JAN-2001; 2001US-0261979P.

17-JAN-2001; 2001US-026194P.

17-JAN-2001; 2001US-0262164P.

17-JAN-2001; 2001US-0262164P.

17-JAN-2001; 2001US-0262169P.

19-JAN-2001; 2001US-026259P.

19-JAN-2001; 2001US-0263066P.

19-JAN-2001; 2001US-0263066P.

19-JAN-2001; 2001US-0263066P.

19-JAN-2001; 2001US-0263066P.
                                                                                                                                                                                                                                                                                             ABS51309 standard; cDNA; 719
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P-PSDB; ABG69816.
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Chang SC,
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The invention describes an isolated polynuclectide a naturally occurring polynucleotide sequence at least 90 % identical to it, a polynucleotide complementary to it or an RNA equivalent of it. The purified secretory polypeptides (SPTW) and polynucleotides are useful in the diagnosis, study, prevention or treatment of diseases associated with decreased expression of functional SPTW, e.g. actinic Keratosis, arteriosclerosis, bursitis, cirrhosis, hepatitis, polycythaemia vera, primary trendscared thrombocytopenia, anaemia, psoriasis, cancers including adenocarcinoma, thrombocytopenia, anaemia, psoriasis, cancers including adenocarcinoma, thrombocytopenia, anaemia, meloma or sarcona, immune system discase mellitus, glomerulonephritis, Goodpasture's syndrome, gout, anahimoto's thyroiditis, hepatitis, multiple sclerosis, osteoporosis, pancreatitis, Reiter's syndrome, autoimmune thyroiditis or rheumatoid arthritis, neurological disorders such as epilepsy, stroke, Alzheimer's disease, plok's disease, Huntington's disease, dementia, Parkinson's disease, plok's disease, Huntington's disease, dementia, Parkinson's disease, other developmental disorder of the central nervous system, mental disorder including mood, anxiety or schizophrenic disorder, annesia or Tourette's disorder. The polynucleotides may be used in hypridiaation and amplification technologies, e.g. in assessing gene expression patterns, to develop a transcript image for a particular cell or tissue, or to create transgenic animals to model human disease. This sequence encodes a human secretory protein isolated in the invention ö 240 300 New purified secretory polypeptides and polynucleotides, useful in the diagnosis, study, prevention or treatment of diseases associated with decreased expression of functional secretory molecules, e.g. AIDS, cancer 593 120 653 Areceaectcagrareccagaaaaarecagaaaaagcaaracaaacreggregacarrac 180 713 773 9 GACCACGGGAGAAGTAGGCATAATGGTTATGAAAGCTTCTGTAGATGATGATGACGATTCAGG CCAAGATTTTGAAGAAGCTTGTCGAGAATTAAAGTTGGGAGAACTACTTCATGATAAGCT ATGGGAGCTCAGTATGCCAGAAAAATGGAGAAAAGCAATACAAACTGGGTGGACATTAC CCAAGATTTTGAAGAAGCTTGTCGAGAATTAAAGTTGGGAGAACTACTTCATGATAAGCT Gaps 0; Length 719; Sequence 719 BP; 223 A; 113 C; 188 G; 195 T; 0 U; 0 Other; Indels DB 6; Score 717.4; DB 6; Pred. No. 5.8e-171; 23.2%; Scc... 99.9%; Pred. No. s.c. ... 0; Mismatches Claim 1; Page 247; 340pp; English. Query Match 23.2 Best Local Similarity 99.9 Matches 718; Conservative or allergies 534 61 594 121 654 181 714 ద ö ò g à g à d 셤

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TTACATTCATAATCCAGACTTTATAGAAGATCCTGCTATGAAGGCTTTTGCTCTGGGAAT

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CATGATTGGAAACCAAGTTAATCGAAAAGTTCTCAATTTTGAACAAGCTATCAAGGATGG

301 834 834 361 894

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AGAITITICAGICAAIGACITAIGGAITITAAAAIGGCIAACAGIGIGACAGAICTICGAGI 1133
      TACAGGCATGCTAAAAGATGTGGAGGATGACATGCAAAGAAGAAGTAAAAGAGTACTCGAA 1192
                                                                                                                                                                       Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                    TACAGGCATGCTAAAAGATGTGGGGGATGACATGCAAAGAAGAGTAAAAGAGTACTCGAA 719
AGALTITICAGTCAATGACTTATGGATTTAAAATGGCTAACAGTGTGACAGATCTTCGAGT
                                                                                                                                                                                                                                                                                                                     Jones LW;
                                                                                                                                                                                                                                                                                                                   Dickson MC,
                                                                                                                                                                                                                                                                                                                    Stache-Crain B,
                                                                                                                                                        Human endothelial cell cDNA #1835
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                                                                                                            ACH33702 standard; cDNA; 482
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LABAT I.
STACHE-CRAIN E
                                                                                                                                                                                                                                                                                           DICKSON M C.
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, it esponsible for genetic disorders and other traits. The nucleotide captences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense PNA or RNA. The purified polypeptide is useful for generating antisense PNA or RNA. The purified polypeptide is useful for generating antisense PNA or RNA. The purified polypeptide for this patent did not form pare of the printed specification, but was obtained in electronic format directly from USPTO at sequence. New polymucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. Claim 1; SEQ ID NO 20914; 44pp; English

Sequence 482 BP; 145 A; 82 C; 124 G; 130 T; 0 U; 1 Other;

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                                                                                                                                                                                                               146 CAGAAAAAATGGAGAAAAAGCAATACAAACTGGGTGGACATTACCCAAGATTTTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 AICTCACCTHGCCTGAACTGATAGGGATTATGGATACATGTTTTTGCTGTTTGATAACGT
                                                              CGAGCTTATTTCCGTGGTCCGGACAGTGCGTGGCGGCGCGGGGTGACCACGGGAGAAGTAG
                                                                                                                            GCATAATGGTTATGAAAGCTTCTGTAGATGACGATTCAGGATGGGAGCTCAGTATGC
                                                                                                                                               86 GCATAATGGTTATGAAAGCTTCTGTAGATGATGACGATTCAGGATGGGAGCTCAGTATGC
                                                                                                                                                                                       CAGAAAAAATGGAGAAAAGCAATACAAACTGGGTGGACATTACCCAAGATTTTGAAGAAG
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                                                                                                                                                                                                                                                                                  206 CTTGTCGAGAATTAAAGTTGGGAGAACTACTTCATGATAAGCTATTTGGTCTTTTTGAAG
                                                                                                                                                                                                                                                                                                                 CCATGTCTGCTATTGAAATGATGGATCCCAAGATGGATGCTGGCATGATTGGAAACCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          851 ATCTCACCTTGCCTGAACTGATAGGGATTATGGATACATGTTTTTGCTGTTTTGATAACGT
                                  Gaps
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   Length
                                Indels
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Wang Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 GGTTAGAAGGCCATTCACTGGCACAGACAGTATTTA 481
Score 451.2; DB 8;
Pred. No. 1.1e-103;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human novel cDNA contig sequence, SEQ ID NO:2051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Ren F, Xue AJ, Zhao QA,
Wang D, Ma Y, Asundi V,
Drmanac RT;
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Query Match
Best Local Similarity 99.3%;
Matches 453; Conservative
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Zhou P, Ghosh M,
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P-PSDB; ADC32736.

treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or New polynucleotide and polypeptide useful for diagnosing, preventing

Example 2; SEQ ID NO 2051; 1185pp; English.

ADC30889 and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an enthod of detecting polynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods to perenting the methods of invention further discloses methods of perenting underlying a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention invention methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32324) and the polymptides encoded by the contigs (ADC32628 ADC33394). The nucleic acids and polypeptides of the invention in the for asserting the responsible for genetic disorders or other for asserting the responsible for genetic disorders or other for asserting the high polymptides or other for asserting the responsible for genetic disorders or other for the formation care. disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a human contig sequence used in an example of the invention. Note: The sequence data for traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at invention relates to 971 novel human cDNA sequences (ADC29919ftp.wipo.int/pub/published_pct_sequences.

Sequence 482 BP; 145 A; 82 C; 124 G; 130 T; 0 U; 1 Other;

ð g à q

0 610 145 670 205 730 265 790 325 850 382 ATCTCACCTTGCCTGAACTGATAGGGATTATGGATACATGTTTTTGCTGTTTGATAACGT 910 85 CTIGICOS GABATTABAGTIGGGAGAACTACTICATGATAAGCTATTIGGTCTTTTTGAAG 86 GCATAATGGTTATGAAAGCTTCTGTAGATGATGACGATTCAGGATGGGAGCTCAGTATGC 146 CAGAAAAATGGAGAAAAGCAATACAAACTGGGTGGACATTACCCAAGATTTTGAAGAAG CCATGTCTGCTATTGAAATGATGGATCCCAAGATGGATGCTGGCATGATTGGAAACCAAG CCATGTCTGCTATTGAAATGATGGATCCCAAGATGGATGCTGGCATGATTGGAAACCAAG TTAATCGAAAAGTTCTCAATTTTGAACAAGCTATCAAGGATGGCACTATTAAAAG GCATAATGGTTATGAAAGCTTCTGTAGATGACGATTCAGGATGGGAGCTCAGTATGC CAGAAAAAATGGAGAAAAGCAATACAAACTGGGTGGACATTACCCAAGATTTTGAAGAAG CTTGTCGAGAATTAAAGTTGGGAGAACTACTTCATGATAAGCTATTTGGTCTTTTTGAAG TTAATCGAAAAGTTCTCAATTTTGAACAAGCTATCAAGGATGGCACTATTAAAATTAAAAG Gaps ., 14.6%; Score 451.2; DB 9; Length 482; 99.3%; Pred. No. 1.1e-103; ive 0; Mismatches 3; Indels 0; Indels Conservative Local Similarity Best Local Sim Matches 453; 551 (326 851 206 731 266 791 611 671 Query Match

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The inversion or muscle and fat deposition (designated IMED), derived from cattle, and the IMED nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 5912 nucleotide sequences, appearing as ABX50072-ABX5593, or complements of them. Also included are included are appearing as ABX50072-ABX5593, or complements of them. Also included are included are included and also included are included and also a promoter and a 3 non-translated sequence that functions in the cell to cause termination of transcription and addition of promoter and a 3 non-translated sequence that the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 end of the mRNA molecule; and close the secretaring a level or pattern of a molecule in a bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) complementary nucleic acid permits the detection of the molecule; and (b) cetecting the level or pattern of the complementary nucleic acid permits the detection of the complementary nucleic acid permits the detection of the complementary nucleic acid sequence confidence acid is used for the detection of the complementary nucleic acid is predictive of the complementary nucleic acid is used for the detection of the complementary nucleic acid is used for the detection of the molecule. The IMPD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breading, preparation of constructs for use in cattle gene expression, or constructs for use in cattle gene expression, or constructs for use in cattle gene expression, or sequence was not shown in the specification but was obtained in cattle format from the USPTO web site:
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of constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                                                                                                                                                                                                                                                                 Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
Bovine EST associated with lactation/muscle/fat deposition #210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purified nucleic acid molecules, useful for genome mapping, identification and analysis, cattle breeding or preparation for cattle gene expression and genetically improved cattle.
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                                                                       GGTTAGAAGGCCATTCACTGGCACAGACAGTATTTA
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                                                                                                                                                                                                                             ABX50281 standard; cDNA; 398 BP.
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(TAON/) TAO N.
(WARR/) WARREN W C.
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                                                                                          TGGTAGCATTTGACATGGACGGCAAAGTACGTAAACCGAAGTTTGAGCTTGATAGTGAAC
                                                                                                                             TGGGAGCTTTTGACATGGATGGCAAAGTACGAAAACCCAAGTTTGAGCTTGATAGTGAAC
                                                                                                                                                                 133 AAGTICGATATGAGCACAGATTTGCTCCATTCAACAGTGTAATGACACCACCACCAGTGC
                                                                                                                                                                                    CTGAACTGTATGTGGCAGCTAGTAAGCACTTTCAACAGGCAAAAATGATATTGGAAAATA
                                                                                                                                                                                                                                         CAGAACTGTATGTGGCAGCTAGTAAGCACTTTCAGCAGGCAAAAATGATACTGGAAAATA
                                                                                                                                                                                                                                                            TICCIAACCCGGACCATGAGGTTAATAGAATTTTAAAGGTTGCCAAACCCAACTTTGTGG
                                                                        AAGTTCGGTATGAACACAGGTTTGCTCCATTCAACAGTGTGATGACCCCGCCGCCAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide for detecting cytosine methylation SEQ ID NO 38250.
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                                    DB 7; Length 398;
                                                       Indels
                 Sequence 398 BP; 131 A; 89 C; 85 G; 93 T; 0 U; 0 Other;
                                            2.7e-78;
hes 22;
 segdata.uspto.gov/sequence.html?DocID=20020137160
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                                   11.3%; Score 350.8;
llarity 94.3%; Pred. No. 2.7e
Conservative 0; Mismatches
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2000DE-01044543,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
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                                           Similarity
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05-SEP-2000;
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                                                                                                            This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convext cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respirators systems etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 IGCICGIICGIGCICGCAACCACIAAGGICIACGCAAACCICCACGGITIICCIICCGCCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide for detecting cytosine methylation SEQ ID NO 38249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 799 BP; 289 A; 297 C; 95 G; 118 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCGGATAGTGCGTGCCGCGCGCGCGTGATTACGGGAAGTAGGTA
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+ Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ51658 standard; DNA; 799
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507

AGTAAGGGAGAGGGGGGGGGGGGGTTTCGGGTATACGTATGCGTGTACGTTGTCGG

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Db ð a à g

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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously, ABQ13410-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ54121 represent genomic DNA sequences used to illustrate the method
drug, side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.1%; Score 343.8; DB 6; Length 799; 83.5%; Pred. No. 2.3e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 799 BP; 118 A; 95 C; 297 G; 289 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                       Guetig D;
                                                                                                                                                                                                                                                                                                                                                                     Berlin K,
                                                                                                                                                                                                                     01-SEP-2001; 2001WO-EP010074.
                                                                                                                                                                                                                                                           01-SEP-2000; 2000DE-01043826.
05-SEP-2000; 2000DE-01044543.
                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                WO200218632-A2
                                                                                       Homo sapiens
                                                                                                                                                                          07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                     olek A,
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cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; ss.

Human prostate expression marker cDNA 15322

13-SEP-2002

ABV15331;

Human; prostate pharmacogenomic

WO200160860-A2

23-AUG-2001

Homo sapiens.

ABV15331 standard; cDNA; 356 BP.

ABV15331,

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2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; determining whether prostate cancer has metastasized in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.4%; Score 292.4; DB 5;
90.5%; Pred. No. 1.5e-63;
iive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 2572; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.5
Matches 344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                 Schlegel R,
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Gaps

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77; Indels

0; Mismatches

Matches 390; Conservative

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TCGCGTTATTTTTAAGAAATTTTTAGAGGTAGCGTAGACGGGGCGGGTTTTGAGATT

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266 181 326

CCGGGCTCCGCCTCTTTCCGGGAACCGCCCACTACCCAGGACTCCGACAGAGGGTGAAAA 122 TCGGGTTTCGTTTTTTCGGGAATCGTTTATTATTTAGGATTTCGATAGAGGGTGAAAA

207

8

d δ qq

62

386

182 AAGATAATTTTCGGTTTTCGCGATCGTTTTTAATTTCGCGAGAAGAGAAGGCGGTCGTTAT CGGCCGAACGGAGGCGGTGGCGAGGGAGGGGGTGTGGCGCGGGGAGCGCGAAGTCCCCGGG

327 242

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267

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

2000US-0255281P

13-DEC-2000;

2000US-0183319P. 2000US-0189862P. 2000US-0207454P. 2000US-0211314P. 2000US-0219007P.

17-FEB-2000; 16-MAR-2000;

25-MAY-2000; 209-JUN-2000; 218-JUL-2000; 2

20-FEB-2001; 2001WO-US005171

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progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) adetermining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGCTTCRCRCCATGCTGTTGAAACAGGAACCCCAAAGGCAACATTTGGCCTTTAGG 105
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marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATAACAAAAAGGTCTTTGGAACTCATCTCATGCAAGACATGGTGAAAGATGCACTTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTTTGTCAGATCCTCCGAGTGCTTTCCCCCAAGTGCTACCTATATAATAATCACCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTAAGGACTGTATCGACTCCTTTGTTACTCACTGTGTTCGGCCATTCTGTAGTCTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u> AGATCCATGGACATAACAGGGCTCGACAGAGAGATAAGCTTGGTCATATTCTTGAGGAAT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATCCATGGACATAACAGGGCTCGACAGAGAGATAAGCTTGGTCATATTCTTGAGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                  Length 439;
                                                                                                                                                                                                                                                                                        Sequence 439 BP; 113 A; 104 C; 110 G; 112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                               9.3%; Score 288.8; DB 5;
llarity 91.4%; Pred. No. 1.4e-62;
Conservative 0; Mismatches 7;
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 338; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate
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18-JUL-2000;
13-DEC-2000;
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16-MAR-2000;
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                                             AAACCACTTTCCGGTGGATAACAAAAAGGTCTTTGGAACTCATCTTGTAGT
                                                                                                                                GAAAGATGCACTTCGGTCTTTTGTCAGATCCTCCGAGTGCTTTCCCCCAAGTGCTACCTA
                                                                                                                                                                       GAAAGATGCACTTCGGTCTTTTGTCAG--TCCTCCGGTGCTTTCCCCCAAGTGCTACCTA
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         AACCACTTTCCTGGTGGATAACAAAAGGTCTTTGGAACTCATCTCATGCAAGACATGGT
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer: (b) monitoring the progression of prostate cancer: (b) monitoring the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                Claim 1; Page 7483; 11750pp; English
                    Monahan JE
                    Endege WO,
                                                                  WPI; 2001-662795/76.
                    Schlegel R,
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Score 288.8; DB 5; Length 439; Pred. No. 1.4e-62; 0; Mismatches 7; Indels 25. Sequence 439 BP; 113 A; 104 C; 110 G; 112 T; 0 U; 0 Other; Query Match

Best Local Similarity 91.4 Matches 338; Conservative

Gaps

25;

1746 1806 1866 380 322 1687 GATAACAAAAGGTCTTTGGAACTCATCTCATGCAAGACATGGTGAAAGATGCACTTCGG GATAACAAAAAAGGTCTTTGGAACTCATCTCATGCAAGACATGGTGAAAGATGCACTTCGG TCTTTTGTCAGATCCTCCGAGTGCTTTCCCCCAAGTGCTACCTATAATAATCACCAGG 379 TCTTTTGTCAG--TCCTCCGGTGCTTTCCCCCAAGTGCTACCTATATAATAATCACCCAGG CTAAGGACTGTATCGACTCCTTTGTTACTCACTGTGTTCGGCCATTCTGTAGTCTTATTC 9.3%; Scort No. 1.1. 91.4%; Pred. No. 1.1. 0; Mismatches 439 1747 1807 ò qq à g δ

TTGCCACCTTGCAGGATG------AGGCAGGAAGGTTGATGC 1867 AGATCCATGGACATAACAGGGCTCGACAGAGATAAGCTTGGTCATATTCTTGAGGAAT AGATCCATGGACATAACAGGGCTCGACAGAGAGATAAGCTTGGTCATATTCTTGAGGAAT TTGCCACCTTGCAGGATGAGTTTATGACATTTTATTAATAGGCAGAGGAAGGTTGATGC 261 1927 201

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321 CTAAGGACTGTATCGACTCCTTTGTTACTCACTGTGTTCGGCCATTCTGTAGTCTTATTC

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164 AGCGCTTCACACCATGCTGTTGAAACAGGAACCCCAAAGGCAACATTTGGCCTGTTTAGG AGCGCTTCACACCATGCTGTTGAAACAGGAACCCCAAAGGCAACATTTGGCCTGTTTAGG 1987

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3225727 seqs, 2453303834 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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3096
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 42, Appl	Sequence 23, Appl	Sequence 20725, A	Sequence 15927, A	Sequence 16155, A	Seguence 3218, Ap	Sequence 9543, Ap	Sequence 20914, A	Sequence 3455, Ap	Sequence 9771, Ap	Sequence 210, App	Sequence 43407, A	Sequence 43407, A	Sequence 5693, Ap
ΩI	US-10-001-857-42	US-10-467-433-23	US-09-814-353-20725	US-09-814-353-15927	US-09-814-353-16155	US-09-814-353-3218	US-09-814-353-9543	US-09-918-995-20914	US-09-814-353-3455	US-09-814-353-9771	US-09-983-965-210	US-10-085-783A-43407	US-10-242-535A-43407	US-09-783-590-5693
DB0	14	17	10	10	10	10	10	10	10	10	თ	13	16	6
* Query Match Length DB ID	3096	2488	2610	745	610	602	602	482	434	434	398	345	345	501
% Query Match	100.0	78.1	72.0	18.1	16.5	16.0	16.0	14.6	14.0	14.0	11.3	9.6	9.6	8.7
Score	3096	2417.2	2228.4	560.8	509.4	496.2	496.2	451.2	434	434	350.8	302.6	302.6	268.6
Result No.	н	7	3	Ω	Ŋ	9 0	0 7	8	6	10	11	12	13	14

Sequence 323193, Sequence 323193,	41,	Sequence 111, App	Sequence 54186, A	5418		44335,	51928,	Sequence 9375, Ap	16495,	96349,	68188,	5998,	1857,	Sequence 1513, Ap	44536,			Sequence 26988, A		64501,	Sequence 2320, Ap	27585,	1481,	Sequence 1189, Ap	Sequence 721, App	1877			Sequence 49515, A
US-10-027-632-323193 US-10-027-632-323193	10-001-857-41	2	US-10-085-783A-54186	US-10-242-535A-54186	US-10-424-599-47623	US-10-437-963-44335	2	ä	-908-975-	10-424-599	2	0-021-323-599	US-10-017-161-1857	0-292-798	2	2	US-10-027-632-31508	US-10-424-599-26988	US-10-424-599-133788	US-10-437-963-64501	US-10-424-599-2320	-10-437-963-27	US-10-017-161-1481	US-10-292-798-1189	US-10-240-425-721	US-10-437-963-18774	US-10-017-161-1403	US-10-292-798-1141	US-10-437-963-49515
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182	140.4	87.8	81.4	81.4	79.2	64.2	60.B	60.2	9	59.8	59.6		00	58.2	28	28	28	57.8	57.4	9.95	56.4	56.2	56.2	56.2	26	26	26	26	55.8
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ALIGNMENTS

RESULT 1

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1014 CTTGAAAATCTGTGACATTGCAAGGGAAAAGTAAATAAAGCTGCTGTTTTTGAAGAGGA 1073
             DISEASE DETECTION AND TREATMENT
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ilarity 98.5%; Pred. No. 0;
Conservative 0; Mismatches
                                     FILE REFERENCE: PF-08899 USN
CURRENT APPLICATION NUMBER: US/10/467,433
CURRENT APPLICATION NUMBER: US/08-06
PRIOR APPLICATION NUMBER: PT/US02/03709
PRIOR FILING DATE: 2002-026
PRIOR FLING DATE: 2002-026
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-03-07
PRIOR FILING DATE: 2001-03-07
PRIOR PILING DATE: 2001-03-07
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
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PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PERL PROGRAM
SEQ ID NO 23
LENGTH: 2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7111920CB1
APPLICANT: MARQUIS, JOSEPH P.
TITLE OF INVENTION: MOLECULES FOR
FILE REFERENCE: PF-0899 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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Matches 2470; Conserv
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                         TGGAATGTTTAAAACCATGGTAGCATTTGACATGGACGGCAAAGTACGTAAACCGAAGTT
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1. YAO, Monique G.; CHAMLA, Narinder K.;
1. YAO, Monique G.; CHAMLA, Narinder K.;
1. ELLIOTT, Vicki S.; XU, Yuming;
1. HONCHELL, Cynthia D.; YUE, Henry;
1. DING, Li, GIEFTERN, Kimberly J.;
1. ISON, Craig H.; LU, Dyung Aina M.;
1. HAPALIA, April J.A.; GANDHI, Ameena R.;
1. TANNG-WELU, Kavitha; SANDAHNALA, Madhusudan M.;
1. TANG, Y. Tom; RAMKUMAR, Jayalaxmi;
1. GRIFFIN, Jennifer A.; SWARNAKAR, Anita;
1. GRIFFIN, Jennifer A.; SWARNAKAR, Anita;
1. BURRORI, Valda; SAPPERSTEIN, Stephanie K.;
1. LU, Yan; TRAN, Uyen K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTATAAAGGTTAATAAATTTCTTGACAAAAAAAAA 3096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: INCYTE CORPORATION;
APPLICANT: LAL, Preeti G.; BAUG
APPLICANT: YAO, Monique G.; CHA
APPLICANT: ELLIOTT, VICKI S.; X
APPLICANT: HONCHELL, CYICKI S.; X
APPLICANT: ING, Li; GIETZEN, K
APPLICANT: ISON, Craig H.; LÜ,
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US-10-467-433-23
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TTACATTCATAATCCAGACTTTATAGAAGATCCTGCTATGAAGGCTTTTGCTCTGGGAAT 1013 360 420 953 480 TTACATTCATAATCCAGACTTTATAGAAGATCCTGCTATGAAGGCTTTTGCTCTGGGAAT CATGATTGGAAACCAAGTTAATCGAAAAGTTCTCAATTTTGGACAAGCTATCAAGGATGG CACTATTAAAATTAAAGATCTCACCTTGCCTGAACTGATAGGGATTATGGATACATGTTT 1 GGCGGCGGCCGAGGCGCGCGTCGTTTCCGTGGTCCGGACAGTGCGTGGCGGGGT GACCACGGGAGAAGTAGGCATAATGGTTATGAAAGCTTCTGTAGATGATGACGATTCAGG ATGGGAGCTCAGTATGCCAGAAAAATGGAGAAAAGCAATACAAACTGGGTGGACATTAC CCAAGATTTTTGAAGAAGCTTGTCGAGAATTAAAGTTGGGAGAACTACTTCATGATAAGCT CATGATTGGAAACCAAGTTAATCGAAAAGTTCTCAATTTTTGAACAAGCTATCAAGGATGG CACTATTAAAATTAAAAGATCTCACCTTGCCTGAACTGATAGGGATTATGGATACATGTTT Gaps

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	ATTCAGCAGAGTGAAATTTACTCGTGTGTTACTGACGAGTGGTTATAGGCGTTTACTAAGAA ATTCAGCAGAGTGAAATTTACTCGTGTGTTACTGACAGTGGTTATAGCCGTTTACTAAGAA ATTCAGCAGAGTGAAATTTACTCGTGTGTTATACTGACAGTGGTTATAGCTAGAAAAAAAA		1021 CCCTCGATATGCAAAATAATTAAAAGGAAGAAATGGTGAACTATTTGCAAGATTAAT 1080 1554 AGATAGAATAAAAACTGTCTGTGAGGTTGTGAATTAACAAATTTACATTGTATCCTGGA 1613 1081 AGATAGAATAAAAACTGTCTGTGAGGTTGTGAATTTAACAAATTTACATTGTATCCTGGA 1140 1614 TTTTTCTGTGAATTTAGTGAAGTGACCATGTGTTTTTAAAATTTAAAATTTACAAAC 1673 1141 TTTTTTCTGTGAATTTAGTGAACAGTCACCATGTGTTTTCAAGAATTTACAAAC 1073	TGAA 173 TGAA 173 TGAA 126 TGAA 126 ATAT 179	ATTC 185 ATTC 137 ATTC 137 FCAT 191 ICAT 143	1914 ATTCTTGAGGATTTGCCACCTTGCAGGATGAGTTTATGACATTTTATTTA

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PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR PLING DATE: 2000-05-15
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NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASELSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 20725
LENGTH: 2610
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LOCATION: 1, 2, 3, 4
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapiens
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Matches 2299; Conser
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TYPE: DNA
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITILE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: MRI-066B
CURRENT APPLICATION NUMBER: US 60/201,124
PRIOR PILING DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: US 60/211,940
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-07-07
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US-09-814-353-15927/c
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Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER;
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER;
FILE REPERENCE: MT.-006B;
CURRENT FILING DATE: 2001-03-21

PRIOR PELING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21
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                                                                                                                                             26;
                                                                                                Length 745;
                                                                                                                                             Indels
                                                                                                DB 10;
                                                                                                                                             8
                                                                                              Query Match
18.1%; Score 560.8; DB 10
Best Local Similarity 94.8%; Pred. No. 1.3e-142;
Matches 621; Conservative 0; Mismatches 8;
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; LOCATION: 571 _
; OTHER INFORMATION: n = A,T,C or
US-09-814-353-15927
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us-10-001-857-42.rnpb

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US-09-814-353-3218
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thille, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                              Length 610;
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                                                                                                                                                                                                                                                                                          Score 509.4; DB 10
Pred. No. 1.4e-128;
0; Mismatches 1;
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PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                          Query Match
16.5%;
Best Local Similarity 99.8%;
Matches 510; Conservative
                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo_sapiens
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Best Local Similarity
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US-09-814-353-3218/c
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                                                                                                                                                                                             SEQ ID NO 16155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.0%; Score 496.2; DB 10
Best Local Similarity 93.9%; Pred. No. 5.8e-125;
Matches 568; Conservative 0; Mismatches 10;
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SEQ ID NO 3218
LENGLAR: 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: 561, 590
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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386 ATCICACCITGCCTGAACIGATAGGGATTATGGATACATGTTTTTGCTGTTTAGATAACGT 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 CAGAAAAATGGAGAAAAGCAATACAAACTGGGTGGACATTACCCAAGATTTTGAAGAAG
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                                                                                                                                                                                    551 GCATAATGGTTATGAAAGCTTCTGTAGATGATGACGATTCAGGATGGGAGCTCAGTATGC
                                          ----AGGCAGAGAAGGTTGATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hyeeq, Inc.
APPLICANT: Hyeeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER: OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 20914, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
| LOCATION: (1)...(482)
| CTHER INFORMATION: n = A,T,C or G
| US-09-918-995-20914
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Matches 453; Conservative
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US-09-918-995-20914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1868 GATCCATGGACATAACAGGGCTCGACAGAGATAAGCTTGGTCATATTCTTGAGGAATT 1927
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US-09-814-353-9543/C

US-09-814-353-9543/C

US-09-814-353-9543/C

Sequence 9543, Application US/09814353

Publication No. US20030165831A1

GRNERAL INFORMATION:

APPLICANT: Thompson, Pamela

APPLICANT: Lillie, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF COVARIAN CANCER

TITLE OF INVENTION: THERAPY OF COVARIAN CANCER

TITLE OF INVENTION: THERAPY OF COVARIAN CANCER

FILE REFERENCE: MRI-006B 1: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR APPLICATION NUMBER: US 60/210,24

PRIOR PLING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR PLING DATE: 2000-05-25

PRIOR FILING DATE: 2000-07-07

PRIOR PLING DATE: 2000-07-07

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Pred. No. 5.8e-125;
0; Mismatches 10; Indels 27;
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NAME/KEY: misc feature
LOCATION: 561, 590
COTHER INFORMATION: n = A,T,C or G
US-09-814-353-9543
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Best Local Similarity 93.9%;
Matches 56%; Conservative (
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ORGANISM: Homo sapiens
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                                                                                                                                 Sequence 3455, 4959

Sequence 3455, 4959

Sequence 3456, 4951

Sequence 3456, 4951

Sublication No. US20030165831A1

GENERAL INFORMATION:
APPLICANT: Lillie, John
APPLICANT: Lillie, James

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: UNBER: US/09/814,353

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

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PRIOR PLICATION NUMBER: US 60/211,940

PRIOR PLILING DATE: 2000-06-15

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PRIOR PLILING DATE: 2000-07-07

PRIOR PLILING DATE: 2000-07-07

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446 GGTTAGAAGGCCATTCACTGGCACAGACAGTATTTA 481
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Matches 434; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                 -09-814-353-3455
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LENGTH: 434
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RESULT 10
US-09-814-353-9771
i Sequence 9771. Application US/09814353
i Publication No. US20030165831A1
i GENERAL INFORMATION:
i APPLICAMT: Lie, John
APPLICAMT: Lilie, James
i TITLE OF INVENTION: DENELS, COMPOSITIONS, KITS, AND METHODS FOR ITILE OF INVENTION: DIBENTIFICATION, ASSESSMENT, PREVENTION, AND ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
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ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
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ITILE OF INVENTION NUMBER: US 60/191,031
FRIOR PILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-06-15
FRIOR APPLICATION NUMBER: US 60/210,920
FRIOR PILING DATE: 2000-07-07
FRIOR PILING DATE: 2000-07-07
FRIOR APPLICATION NUMBER: US 60/220,661
FRIOR PILING DATE: 2000-07-07
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100.0%; Pred. No. 5.3e-108;
tive 0; Mismatches 0;
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US-09-814-353-9771
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Best Local Similarity
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##FILICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005

CURRENT PEPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

SEQ ID NO 43407

LENGTH: 345
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97.3%; Pred. No. 5.2e-72;
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APPLICANT: ChondroGene Inc.
                                                                                                                                                                                                                                                          LOCATION: (16)...(16)
COTHER INFORMATION: n is a, c, g, or US-10-085-783A-43407
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LOCATION: (16)...(16)
OTHER INFORMATION: n is a, c, g,
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/;
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SCOFTWARE: Patentin version 3.2
SEQ ID NO 43407
LENGTH: 345
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ORGANISM: Human
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ORGANISM: Human
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                                                                                       APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERRNCE: 37-21(10297)C
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
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Publication No. US20040037841A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chondrodene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR PLING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
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US-09-983-965-210
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                        Sequence 210, Application US/09983965
Patent No. US20020137160A1
GENERAL INFORMATION:
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US-10-085-783A-43407
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...aseltine Teleson, Craig A.
...applicant: Rosen, Craig A.
...applicant: Rosen, Craig A.
...applicant Policy B.
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                                                                                                          Gaps
                                                                                                            4;
                                                     DB 16; Length 345;
                                               9.8%; Score 302.6; DB 16; Length 97.3%; Pred. No. 5.2e-72; Live 0; Mismatches 5; Indels
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NAME/KEY: misc feature
LOCATION: (289)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (315)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (383)
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                                                                                                       Conservative
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ORGANISM: Homo sapiens
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LOCATION: (226)
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                                                                          Similarity
US-10-242-535A-43407
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US-09-783-590-5693
                                                                            Best Local Sim
Matches 329;
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2462 ACCCCGCCGCCAGTGCACTACTTACAGTT--CAAGGAAATGTCTGACCTCAATAAATATA 2519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2403 AGCTT-GATAGTGAACAAGTTCGGTATGAACACAGGTTTGCTCCATTCAACAGTGTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 AGCTIGGTIAGIGAACAAGTICGGIAIGAACACAGGTIINCICCATICAACAGIGIGAIG
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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93.2%; Pred. No. 1.5e-62;
tive 0; Mismatches 17
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OTHER INFORMATION: n equals a,t,g, or
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                                                                                      LOCATION: (403)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
n equals a,t,g,
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NAME/KEY: misc feature
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                                LOCATION: (390)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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Best Local Similarity 93.2
Matches 313; Conservative
               misc feature
                                                                     NAME/KEY: misc feature
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US-10-027-632-323193/c
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1551 AATAGATAGAATAAAAACTGTCTGTGAGGTTGTGAATTTAACAAATTTACATTGTATCCT 1610
281 AATAGATAGAATAAAAACTGTCTGTGAGGTTGTGAATTTAACAAATTTACATTGTATCCT 222
                                                                                                                                                                                                                                                                                                                                                                    1431 AGATCATCCAATTATGATGGGTTTTTGAACCCCTTGTGAACCAGAGGCTACTTCCACCTAC 1490
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GG 1612
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; ORGANISM: Human
US-10-027-632-323193
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Search completed: August 11, 2004, 13:00:44 Job time : 1439.92 secs

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Query Match
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Sequence 11, Appl
Sequence 14, Appl
Sequence 7, Appli
Sequence 12, Appl
Sequence 12, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 16, Appl
Sequence 16, Appl
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Sequence 17, Appli
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Sequence 4145, Ap
Sequence 4115, Ap
Sequence 1215, Ap
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Sequence 14, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 6, Appli
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                                                                                              (without alignments)
7635.278 Million cell updates/sec
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                                                                                 August 10, 2004, 17:10:22 ; Search time 225.025 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-543-681A-4140
US-09-543-681A-4145
US-09-543-681A-4115
US-09-023-655-1215
US-09-023-655-1215
US-09-09-894-844-14
US-09-909-962A-6
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US-09-165-264-11
US-09-165-264-14
US-09-165-264-13
US-09-165-264-12
US-09-165-264-12
US-09-165-264-8
US-09-165-264-8
US-09-165-264-8
US-09-165-264-8
US-09-165-264-12
US-09-1165-16
US-09-128-155-16
US-09-128-155-16
US-09-16-289-45
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US-09-16-289-45
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US-09-103-840A-1
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                                                                                                                                                                                                                                         682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
                                                                                                                                       US-10-001-857-42
3096.
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Match Length DB
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1.7 2561 4

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Perfect score:
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Sequence 29, Appl
Sequence 4147, Ap
                      Sequence 3, Appliance 11, Appl Sequence 11, Appl Sequence 181, Appl Sequence 176, App Sequence 181, Appl Sequence 9, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance 181, Appliance
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                 US-09-470-443-3
US-09-091-952A-29
US-09-543-681A-4147
US-09-007-005-17
                                             US-08-458-568A-11
US-09-621-976-2813
US-09-056-556-181
US-09-072-596-176
US-09-072-596-191
US-09-37-54-9
US-09-470-443-7
US-09-312-038-4
US-09-312-038-4
US-09-850-964-4
US-09-850-964-3
US-09-850-964-3
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Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ITTLE OF INVENTION: R.E.OMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BRIT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEFROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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LENGTH: 7218 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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CLONE: pTZqpt-
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COUNTRY: USA
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Length 7218;

DB 1;

2.2%; Score 69.4;

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RESULT 3
US-09-165-264-14
                                                                                                                                                                                                                     SEQ ID NO 14
LENGTH: 320
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US-09-165-264-7
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                                                                                                                                                                                                                                                                                                663 TGAAGAAGCTTGTCGAGAATTAAAGTTGGGAGAACTACTTCATGATAAGCTATTTGGTCT 722
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Pred. No. 7.5e-06;
0; Mismatches 131; Indels
  ilarity 5.9%; Pred. No. 1.3e-08;
Conservative 235; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 50.8'
Matches 135; Conservative
Best Local Similarity
Matches 25; Conserva
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483 CGAGGCGGCGTCGTTTTCCGTGGTCCGGACAGTGCGTGGCGGCGCGCGGGTGACCACGGG 542
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COTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55.2; DB 3; Length 320;
Pred. No. 1.6e-05;
0; Mismatches 138; Indels
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                                                                                                                                                                                                                                                                                      APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
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TITLE OF INVENTION: Multi-Loci Genomic Anal
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SSOTYMARE: PatentIn Ver. 2.1
LENGTH: 320
                                                                   543 AGAAGTAGGCATAATGGTTATGAAAG 568
                                                                                                             292 GGGGGGGGGAGATTTTGAAGAAG 317
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT PILLING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                       Sequence 14, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 50.0%;
Matches 138; Conservative (
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US-09-165-264-8
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 Score 54.8; DB 3; Length 320;
Pred. No. 2.1e-05;
0; Mismatches 122; Indels
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
ETLE REPERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09165264 Patent No. 6197510 GENERAL INFORMATION:
1.8%;
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Matches 128, Conservative
             Best Local Similarity 51.2
Matches 128; Conservative
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US-09-165-264-13
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LENGTH: 320
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US-09-165-264-12 ; Sequence 12, Application US/09165264

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 GCCGGGGAGCGCGAAGTCCCCGGGAGTAAGGGAGAGGGGGGCGGGTCGCGCGTCCCGGGC
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; Patent No. 6197510
; GENERAL INFORMATION:
GENERAL INFORMATION:
; APPLICANT: Vinayagamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44447
; CURRENT APPLICATION UNMBER: US/09/165,264
; CURRENT APPLICATION UNMBER: US/09/165,264
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; Patent No. 6197510;
; GENERAL INFORMATION:
APPLICANT: Vinyagamoorthy, Thuraiayah
; TITE OF INVENTON: Multi-Loci Genomic Analysis;
FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO. 12
LENGTH: 318
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                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                             1.8%; Score 54.2; DB 3; 50.2%; Pred. No. 3.1e-05;
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                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Matches 134; Conservative
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Best Local Similarity
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NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 GECCECCATCGGCCGAACGGAGGCGGTGGGGGGGGTGTGGCCGGGGAGCGCGAA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                              378 GTCCCCGGGAGTAAGGGAGAGGGGCCGGGGTCGCGCGTCCCGGGCATACGCATGCGTGCA
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                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09103840A

Sequence 2, Application US/09103840A

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: USDATER, John C.
TITLE OF INVENTION: THERCULOSIS
FILE REPERBNCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION:
FILE REFERENCE: 24366-20007.00
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1.8%; Score 54.2; DB 3; Length 4
Best Local Similarity 52.4%; Pred. No. 0.016;
Matches 119; Conservative 0; Mismatches 108; Indels
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US-09-103-840A-2
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US-09-103-840A-1
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APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-07-14

PRIOR PLILING DATE: 1997-11-26

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PRIOR PRIL
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CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                          LENGTH: 4411529
TYPE: DNA
ORGANISM: Wycobacterium tuberculosis
THER INFORMATION: H37Rv
US-09-103-840A-1
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Patent No. 6632923
                                         1998-06-24
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52.8%;
                                CURRENT FILING DATE: 1998-INUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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US-09-616-289-48
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Best Local Similarity
Matches 115; Conserva
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Matches 119; Conserv
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GENERAL INFORMATION:
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US-09-616-289-48/c
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ORGANISM: Homo sapiens
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395 AGAGGGGGGGGGTCGCGCGTCCCGGGCATACGCATGCGTGCACGCTGCCGGTCGGGCTG 454
                                                                                  801 GCGCGGGCGGCGCGCCGGCCAGGGCGCGCGCCGCTGCGCGCGGGGGCCCCGGCTGCGCGG 742
                                                                                                                                                                          GGCTGAGAGGGGAGGGGGGGGGGGGGGGGGGGGGTCGTTATTTCCGTGGTCCGGAC 514
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APPLICANT: Pan, Yang
TITLE OF INVENTION:
AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
BARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Ariona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
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                                                                                                                                                                                                                                                                                                                                               515 AGTGCGTGGCGCGCGCGGTGACCACGGGAGAAGTAGGC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 45, Application US/09616289; Patent No. 6632923; GENERAL INFORMATION:
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US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
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SEQ ID NO 16
LENGTH: 152331
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US-09-616-289-45/c
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GEMERAL INVEXABLICUM:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: NOWBER: US 09/517,849

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 1997-11-26

PRIOR PPLICATION NUMBER: US 60/031,930

PRIOR PPLICATION NUMBER: US 60/031,930

PRIOR PPLICATION NUMBER: US 60/031,930

PRIOR PPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1997-11-26

PRIOR PPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FBRESQ FOR Windows Version 4.0

SEQ ID NO 50

LENGTH: 12425

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Pred. No. 0.0013;
0; Mismatches 105; Indels
THIE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1614
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Best Local Similarity 53.9°
Matches 124, Conservative
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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LOCATION: (1)
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US-09-616-289-45
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LENGTH: 4403765
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US-09-103-840A-2/c
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                                                                                   315 GGCGGCCGCCATCGGCCGAACGGAGGCGGTGGCGAGGGAAGGGGGTGTGGCCGGGGAGCGC
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                          Score 50; DB 4; Length 12425; Pred. No. 0.0051;
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                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09773816
; Sequence 1, Application US/09773816
; Patent No. 6340774
; GENERAL INFORMATION:
; APPLICANT: Stanford University
; APPLICANT: Stanford University
; APPLICANT: Khosla Chaitan
; TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; FILE REPRENCE: 28600-20210.00
; CURRENT RILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 60/243,458
; PRIOR PILING DATE: 2000-10-25
; PRIOR PILING DATE: 2000-10-25
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1
; NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176;
                                                        0; Mismatches 105;
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Pred. No. 0.022;
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OTHER INFORMATION: n = A,T,C or G
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Similarity 46.7%;
54; Conservative (
                                                        Conservative
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                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ID NO 1
LENGTH: 23673
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US-09-616-289-50
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                                                        124;
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US-09-773-816-1
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4767 GGCCCGCGAACGACGCCGCGGGCCGGGCGGGGTGTTCGCGTACCGCGAGGCGGGG 4708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Pred. No. 1.3;
0; Mismatches 111;
                                                                                                             4707 ccegecccesaacesarerecesaces 4678
                                                         511
                                                         482 CCGAGGCGCGTCGTTATTTCCGTGGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various
OTHER INFORMATION: represent a, t, c or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                    Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.5%;
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT
APPLICANT: WHITE, OWEN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.7
Matches 114; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model - protein search, OM protein

on:

August 10, 2004, 21:49:02; Search time 20 Seconds (without alignments) 3525.419 Million cell updates/sec

US-10-001-857-145 3849 Title: Perfect score:

1 MVMKASVDDDDSGWELSMPE.....KVPPEFDFSAHKYFPVVKLV Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	hypothetical prote		- ⊆	hypothetical prote	-	hypothetical prote	III res	NMD2 protein - yea		hypothetical prote	tic	vitellogenin vit-5	KIAA0729 protein -	hypothetical prote	dystrophin, muscle	transcription fact		n vit-		RESA-H3 antigen PF	hypothetical prote		hypothetical prote	hypothetical coile	TEL1 protein - yea	hypothetical prote	NMDA receptor-bind	hypothetical prote	hypothetical prote
SUMMARIES	OT .	44	T32223	531288	T39742	SJHUA	S20106	E71810	S48244	T16111	T21982	T30336	VJKWS	T13057	T02576	S02041	T00023	T21328	F89497	JC4013	B71603	S48385	T05384	T43446	T38077	S45416	S46715	T08880	_	T23103
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	Length	695	814	733	708	2429	1152	696	1089	778	1607	2253	1603	1196	1029	3660	736	3147	1603	1023	1558	1679	719	833	1957	2787	4	1642	m	1133
ď	% Query Match	ഥ	14.2	7.0	9.9		3.4	3.3	э.	3.2	3.2	3.2	3.2	3.1	3.1	3.1	3.0	3.0	М	e	m	m.						2.9		
	Score	584	548	270.5	252.5	13	132.5	127	127		122.5	122.5	121.5	119	118.5	117.5	116	11	114.5	114	114	114	113.5	113.5	113.5	113	17	112.5	112	
	Result No.	i	0	m	4	Ŋ	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypoxia-inducible	hypothetical prote	kinesin-like prote	hypothetical prote	M protein precurso	kinesin-related pr	nucleotide-binding	hypothetical prote	translation initia	reverse transcript	hypothetical prote	DNA polymerase III	translation activa	intracellular prot	serine/threonine-s	BNI1 protein - yea
JC4851	S48326	S33417	T49752	A60115	A48669	861535	T16613	T50773	S65824	T21172	C82898	A48126	D69171	870633	S63244
N	~	α	N	7	Н	N	~	7	7	7	7	7	7	7	C)
1505	209	1067	601	564	1066	1620	2427	900	1275	1576	1442	2672	837	1388	1953
15															
2.9 15	2.9	2.9	2.9	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	2.8	7.8
2.9										109 2.8				108 2.8	108 2.8

		[imported]
		At2g11000
		protein
7 7 7 7 7 7	4495	pothetical

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-695 <STO>

A; Cross-references: GB: AE002093; NID: 94662644; PIDN: AAD26914.1; GSPDB: GN00139

A, Gene: At2g11000 A, Map position: 2

25; Query Match 15.2%; Score 584; DB 2; Length 695; Best Local Similarity 23.5%; Pred. No. 1.1e-35; Matches 184; Conservative 153; Mismatches 291; Indels 156; Gaps

96 09 | : : | : | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | : | | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 3 MKASVDDDDSGWELSMPEKMEKS-----NTNWVDITQDFEEACRELKLGELLHDKLFGL à 셤 111 61 FAAMSALEIMDPKMDSGWVST----FYSIDEAIESGFAPVPISSDSTVNVQSIIDIMDH 115 57 FEAMSAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKI-----KDLTLPELIGIMDT à

112 CFCCLITWLEGHSLAQTVFTCLYIHNPDFIEDPA-MKAFALGILKICDIAREKVNKAAVF 170 qq à

gg

171 BEEDFQSMTYGFKMANSVTDLRVTGMLKDVEDDMQRRV---KSTRSRQGEERDPEVE--- 224 Dp à

232 SNPHLEESFCKSLLCRIRFRKHFLHALNCMRRPQGRGLELARKHIGYCISELDSVLDSAE 292 ----LEHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNS--ò

g

----LHHGIQ--AQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFA 330 FLRLDIFENGVNEIEESTTASGRSPI--GFDPTLNKRLSAPTPPRAIKLLSWKKAIDYYV 350 ð dd RLIDRIKTVCEVVNLTNLHCILDFFCEFSBQSPCVLSRSLLQTTFLVDNKKVFGTHLMQD 390 :|: : :| :|:| :| :|-| :| :|-| :| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-| :|-331 à

ò	391 MUKDALRSFVDPPVLSPKCYLYNNHOAKDCIDSFVTHCVRPFCSLIOIHGHNRARO 446	qQ	1 : 214 LEI
7		Ì	
g B	405405	λŏ	255 TSA
ζö	447 RDKLGHILBEFATLQDBFMTFYFNRAEKVDAALHTMLLKQEPQRQHLACLGTWV 500	qq	274 TTE
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δλ	501 LYHNLRIMIQYLLSGFELELYSMHEYYYYIXWYLSEFLYAWLMSTLSRADGSQMAE 555	qq	333 ETV
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ò	556 ERIMEEQQKGRSSKKTKKKKVRPLSREITMSQAYQNMCAGMFKTWVAFDMDGKV 610	qa	393 IYH
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ò	611 RKPKFELDSEQVRYEHRFAPFNSVMTPPPVHYLOFKEMSDLNKKSPPPQSPELYVAASKH 670	qq	: 447 SIA
Db	576 LKSQGPFNTENEKFIQHFELLQKASLPEYDAYESFSKSTSHARLDYLPMYEY 627	λŏ	447 RDK
δ	PDHEVNRILKVAKPNFVVMKLLAGGH	qa	11: 507 RDR
QQ	628 FHDAQKIAKDIKVGYANDPDKLAEVTGLEKVAERNIVAVNLFCQDRSLKVSFEFTH 683	λō	505 LRI
ò	724 HKYF 727	qq	562 LAI
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C;Specie		qq	: 675 KMP
C; Access	Z3-UCC-1999 #sequence_revision 29-UCC-1999 #rexr_cnange z1-Uan-z000	ò	670 HFC
k;Davidi submitte A;Descri	Kidavidson, S.; Monidmann, F.; Gillam, B. submitted to the EMBL Data Library, September 1997 A.Description: The sequence of C. elegans cosmid T23B12.	qq	733 SFN
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A;Cross- A;Experi	references: EMBL:AF022982; PIDN:AAB69936.1; GSPDB:GN00023; CESP:T23B12.4 .mental source: strain Bristol N2; clone T23B12	C,Speci C,Date:	es: Sacche 28-May-19
C;Geneti A;Gene:	C;Genetics: A;Gene: CESP:T23B12.4	C,Acces R,Lee,	sion: \$312 Y.J.; Wic
A; Map po	A;Map position: 5 A;Introns: 24/1; 70/3; 468/2; 543/1; 616/1; 714/2	Genetic A:Title	s 132, 87-
C;Superi	amily: Caenorhabditis elegans hypothetical protein T23B12.4	A; Refer	ence numbersion: S312
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δλ	18 MPEKMEKSNINWVDITQDFEEACRELKIGELLHDKLFCLFEAMSAIEMMDFKMDAGMIGN 77	Submitt A.Refer	ed to the
qq	1 MPGAMESPNES-EDVSKTFFKLCDGLRLGELVTTEHFRLSDVMSAIELGRPKMDVG-VG- 57	A; Acces	sion: S308
δ	78 QVNRKVINFEQAIKDGTIKIKDLTLPBLIGIMDTCFCCLITWLEGHSLAQTVFTCLYIHN 137	A,Resid	lues: 1-733
οg	58SKHIKTLKEAISGG-LYADDYPFQLAIMDSTLAMVVAMLEGSALGSTVWTNVLLSN 112	R;Ciosa R;Dietr	ich, F.S.
δÿ	138 PDFIEDPAMKAFALGILKICDIAREKVNKAAVFEBEDFQ-SMTYGFK 183	A; Refer	iption: The
Dp	113 VTFVKHPVFHPFASGVNLFIRNAHALLNSVGNLBELPEDFNPQMLFSHQRWAPRRVVVQL 172	A; Molec	sion: S504
ζ	MANSVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVL	A; Resid A; Cross	A; Residues: 1-733 A; Cross-reference
Dp	173 MREQVTLLGTTGRKWRESAFSKQAYDICCAVASRLEMFIML 213	C;Genet A;Gene:	ics: SGD:MAK10
ð,	244 LTVLIAFTKKE 254	A, Cross	-reference

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yeast (Saccharomyces cerevisiae)

es: protein YEL053c haromyces cerevisiae 1993 #sequence_revision 28-May-1993 #text_change 21-Jul-2000 1288; 830824; 850491 Ckner, R.B. 7-66, 1993 a glucose-repressible gene necessary for replication of a dsRNA virus of ber: 831288; MUID:93012936; PMID:1398065

33 <LEE>
ces: EMBL:M94533; NID:g171874; PIDN:AAA34749.1; PID:g171875
ti Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, I.
EMBL Data Library, February 1993
ber: S30812

3 <MUL>

es: GB:U18779; EMBL:L10830; NID:g603625; PID:g603626

EMBL Data Library, December 1994
The sequence of S. cerevisiae cosmids 8199, 8334, per: S50491

and 9871

33 <DIE>
ces: EMBL:U18779; NID:g603625; PID:g603626; MIPS:YEL053c

10 ces: SGD:S0000779; MIPS:YEL053c

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 1.7-May-1985 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C; Date: 1.7-May-1985 #sequence_revision 30-Jun-1992; A22875; A23865; A276
C; Accession: A35716; A45755; A23533; A91528; A42872; A2655; S13138; A05282; A23865; A276
R; Sahr; K.E.; Laurila, P.; Kotula, L.; Scarpa, A.L.; Coupal, E.; Leto, T.L.; Linnenbach, A. Baol. Chem. 255, 4434-4443, 1990
A; Title: The complete cDNA and polypeptide sequences of human erythroid alpha-spectrin. A; Reference number: A35716; MUID:90170949; PMID:1689726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQPIRVDFS---RDLSYLEILALMDLIVSAEKEWHYGSPLSESLLCSAHVFSICKSPISQ 140
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                                                                                                                                                                                                                                                     26 NTNWVDITQDFEEACRELKLGELLHDKLFGLFEAMSAIEMMDPKMDAGMIGNQVNRKVLN 85
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ilarity 18.7%; Pred. No. 8.3e-11;
Conservative 143; Mismatches 302;
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502 EQKLHQPYQWPHFFAVL--
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A; Molecule type: mRNA
A; Residues: 1-2429 <SAH>
                                                                                                                                           Local Similarity
les 143; Conserv
                                     A; Introns: 565/3
       A; Map position:
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A;Cross_references: EMBL.AL109834; NID:e1536510; PIDN:CAB52739.1; GSPDB:GN00067; SPDB:SF
A;Cross_references: Extrain 972h-; cosmid c1861
C;Genetics:
A;Gene: SPDB:SPBC1861.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 DVVINSLT-----ESLÖILEAYSDDSLHL 215
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                                                                                                                                                                                                                                                         VDITQDFEEACRELKLGELLHDKLFGLFEAMSAIEMMDPKWDAGMIGNOVNRKVLNFEQA 89
                                                                                                                                                                                                                                                                                                      20 VDVTSLFDELCSKLKPEAIVKDPRFDLFEGTHSLEVNNSKLDSSLI--ELTAEEIEFDVN 77
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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R;Oliver, K.; Harris, D.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                     90 IKDGTIKIKDLTLPELIGIMDTCFCCLITWLEGH-SLAQTVFTCLYIHN----
                                                                                                         Length 733;
                                                                                                      Query Match 7.0%; Score 270.5; DB 2; Best Local Similarity 19.7%; Pred. No. 3.9e-12; Matches 134; Conservative 121; Mismatches 270;
A;Map position: 5L
C;Superfamily: Saccharomyces cerevisiae MAK10 protein
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A;Molecule type: DNA
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A;Accession: T39742
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Matches 175; Conserv
F;1394-1498/Domain: s;
F;1499-1604/Domain: s;
F;1605-1710/Domain: s;
F;1711-1816/Domain: s;
F;1817-1925/Domain: s;
F;21926-2032/Domain: s;
F;2155-2257/Domain: s;
F;2155-2257/Domain: c;
F;2270-2302/Domain: c;
F;2270-2302/Domain: c;
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A. Title is Sequence and exon.intro organization of the DNA encoding the alphal domain of Accession. A4575; will:9009318; PMID:2794061

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C'Genetics:
A;Gene: GDB:SPTA1
A;Cross-references: GDB:119601; OMIM:182860
A;Gene: GDB:SPTA1
A;Cross-references: GDB:119601; OMIM:182860
A;Gene: GDB:SPTA1
A;Cross-references: GDB:119601; OMIM:182860
A;Map position: 1421-1421
C;Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/dystrophin repeat homology <SP2>
C;Superfamily: spectrin/dystrophin repeat homology <SP3>
F;157-262/Domain: spectrin/dystrophin repeat homology <SP3>
F;263-368/Domain: spectrin/dystrophin repeat homology <SP3>
F;360-474/Domain: spectrin/dystrophin repeat homology <SP3>
F;361-685/Domain: spectrin/dystrophin repeat homology <SP3>
F;363-369/Domain: spectrin/dystrophin repeat homology <SP3>
F;364-6791/Domain: spectrin/dystrophin repeat homology <SP3>
F;364-1031/Domain: spectrin/dystrophin repeat homology <SP1>
F;364-1031/Domain: spectrin/dystrophin repeat homology <SP1>
F;188-1287/Domain: spectrin/dystrophin repeat homology <SP1>
F;188-1288-1393/Domain: spectrin/dystrophin repeat homology <SP1>
F;1288-1287/Domain: spectrin/dystrophin repeat homology <SP1>
F;1288-1393/Domain: spectrin/dystrophin repeat homology <SP1>
F;1288-1
       A;Cross-references: GB:J05244
KSahr, K.E.; Tobe, T.; Scarpa, A.; Laughinghouse, K.; Marchesi, S.L.; Agre, P.; Linnent
J. Clin. Invest. 84, 1243-1252, 1989
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1888 VLHEES------QNKEISSKIBALNEKTPSLAKAIAAWKLQLEDDYAFQEFNWKADVV 1939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 EAQKIMVQ--AADLLSAI-----HNSLH-----HGIQAQNDTTKGDHPIMMGFEPLVNQ 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1572 GNEEAMKEQLEQLKEHWDHLLERTNDKGKKLNEASRQQRFNTSIRDFBFWLSEAETLLAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1721 IDDEESWIEBKLIRVSSQDYG-RDLQGVQNLLKKHKRLEGELVAHEPAIQNVLDMAEKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 STRSRQGEERDPEVEL----EHQQCLAVFSRVKFTRVLLTV----LIAFTKKETSAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LSGFEL-ELYSMHEYYYIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GWELSMPEKMEKSNTNW---VDITQD----FEEACRELKLGELLHDKLFGLFEAMSAIEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 MDPKMDAGMIGN-----QVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCLITW
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           280;
                                                                                                                                                                                                                                                                                                                                                                            3.5%; Score 134; DB 1; Length 2429;
                                                                                                                                                                    <SP18>
                                                                      <SP15>
                                                                                                     <SP16>
                                                                                                                                     <SP17>
                                                                                                                                                                                                                                <SP20>
   <SP13>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1836 EKNALAVRGDCGDTLAATQSLLMKHEALENDFAVHETRVQNVCAQG
                                                                                                                                                                    homology
homology
homology
                                                                                                     homology
homology
       homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1632 KDQARDLASAGNILKKHQLLEREMLAREDALKDLNTLAEDL
                                                                         homology
                                          homology
                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 19.4%; Pred. No. 0.37;
Conservative 142; Mismatches 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998 OHNOSKAIEERYAALLKRWEQLLEASAVHROK---
                               .. spectrin/dystrophin repeat ho

.. spectrin/dystrophin repeat ho

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spectrin/dystrophin repeat
                                                                                                                                                                                                                                                                          calmodulin repeat homology
                                                                                                                                                                                                                                                                                                      calmodulin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 LG-----TWVLYHNLRIMIQYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 LSRSLLQTTFLVDNKKVFGTHL-
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qa	2331 GYVSLEDYTAFLIDKESENIKSSDEIENAFQALAEGKSYITKEDMKQALTPEQV 2384	QY 275 IHNSLHHGIQAQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRXAKIIKREE 324
ζλ	720 DFSA 723	Db 626 INNSLSKSFTSKRGTKQGDPISPTIFALVVECMATTIINDRCINGVTKETIKILQFADDT 685
qq	2385 SFCA 2388	QY 325MVNYFARLIDRIKTVCEVVNLTNLHCILDFFCEFSEQSFCVLSRSLLQTT 374
RESULT 6 520106	Propertion protein 2 - slime mold (Dictyostellum discoideum) retrotransposon DRE 522006 Chopsochestical protein 2 - slime mold (Dictyostellum discoideum) retrotransposon DRE 522006 Chopsochestical protein 2 - slime mold (Dictyostellum discoideum) retrotransposon DRE 522006 E. Marschlake, E., McKeman, J.; Schwaman, G.; Goesseringer, B.; Dingeramn, T. Allile: Structure of BEE, a retrotransposeble element which integrates with position sp. A. Accession: \$20106; \$8320999	09 315 FUNDKKVPGTHLANDANFOLALSEVULYSEKCYLYNDHQAKDCIDSPYTEKURPC- 433 Db 733 VISSERIGEPRENKGIGSKRITISD- 18-KYTNANGLANDALTHALAGE 477 Db 734 VISSERIGEPRENKGIGSKRITISD- 18-KYTNANGLANDALTHALAGE 477 Db 735 VISSERIGE FOR THE THE THE THE THE THE THANGLANDALTHALAGE 477 Db 826 SEQUENCE THE THANGLANDALTHALAGE AND THANGLANDALTHALAGE 477 Db 826 SEQUENCE THANGLANDALTHALAGE AND THANGLANDALTHALAGE 477 Db 826 SEQUENCE THANGLANDAL SIGNAL AND THANGLANDALTHALAGE AND THANGLAND 607 Db 826 SEQUENCE THANGLANDAL SIGNAL AND THANGLANDALTH SELVANDALTH SETULATION 607 Db 826 SEQUENCE THANGLANDAL SIGNAL 678 DD 826 SEQUENCE THANGLANDAL SIGNAL 678 DD 930 JOLKEROL SEQUENCE THANGLANDAL SIGNAL 678 DD 946 SEQUENCE THANGLANDAL SIGNAL 678 DD 946 SELVANDAL 678 DD 946 SELVANDAL 678 DD 947 SERVENCE SIGNAL 678 DD 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----RVTGM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 KDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537
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hypothetical protein F20D12.4 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C.Accession: T16111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRNTGFIKKLKKGFVKGSESSLLKDLSEASLEKYLSEIIVTVTECLLNVLNKNDDVIAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PDFIE-----DPAMKAFALGILK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 IFFSEMIK------FQLIPSFMIFHKIRTLIMYMQVPNNVEILTV-----LLEHSGKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LNKPEYKELMEKMY-------QLIKDKKNDRQLN--MNMKSALENIITLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 AKIIKREEMVNYFARLIDRIKTVCEV-----VNLTNLHCILDFFCEFSEQSPCVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 SRSLLQTTFLVD--NKKVFGTHLMQDMVKD-ALRSFVDP-----PVLSPKCYLYNNHQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --NKINVKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 ALHTMLLKQEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 222;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIISGLHQRFNGRFTSPLLG------AFLQAFENPSVDIES-ERDEL
A;Cross-references: EMBL:U28158
R;Varmus, H.E.
submitted to the EMBL Data Library, May 1995
A;Reference number: $64738
A;Accession: $64738
A;Molecule type: DNA
A;Residues: "MYQQ',3-1089 <VAR>
A;Cross-references: EMBL:U28158; NID:g967212; PID:g967213
C;Genetics:
A;Genetics:
A;Genetics: A;Genetics: A;Amap position: 8R
A;Introns: 2/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ICDIAREKVNK-AAVFEEED---FQSMTYGFKMANSVTDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSNTNWV-------DITQDFEEACRELKLGELL
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.3%; Score 127; DB Best Local Similarity 17.6%; Pred. No. 0.4; Matches 117; Conservative 124; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           +41 PEIVSEFINYLDNGFRS--QLHS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITWLEGHSLAQTVFTCLYIHN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKTMV 602
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548244
NMD2 protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: IFS1 protein; protein YHR077c
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence revision 10-Feb-1995 #text_change 23-Mar-2001
C;Accession: S4824; S46815; S64648; S64738
R;He, F.; Jacobson, A.
submitted to the EMBL Data Library, September 1994
A;Description: Identification of a novel component of the nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578
                                                                                                                                                                                                                                                                     -----RIKTVCEVVNLTNLHCILDFFCEFSEQSPCVLSRSLLQTTFLVDNKKVFGTHLMQ 389
                                                                                                                                                                                                                                                                                                                                                                                                                                              404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAE----KVDAALHTMLLKQEPQ 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFLYAW----LMSTL 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LILKEKEKLLSFDSDL----RFIFSQWALQE---GWDNPNVMTIC 494
                                                                                                                                                                                                                                                                                                                                                                                                                             TNLFNGAKSYMQALASMRPIVIMDEPHRFLGDKTKKYLEQLNAL-ITLRFGATFKDDY--
                                                                                                                                                                                                                                                                                                         294 KIQSVKVKTHDNLGALTHISALEDYIVEKITKTEI---RFLNGFNLLLDQKEPP-SHLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623 RYEHRFAPFNSVMTPPP-----VHYLQFKEMSDLNKYSPPPQSPELYVAASKHFQQAK
                                                                                                                                                                                                             --HNLIYALD---SKKAFDCALVKSISVASVGESDEYFLELKEANKKONEATINYTTLEN
                                                                                                                                                                                                                                                                                                                                                                                   D----MVKDALRSFVD-----PPVLSPKCYLYNNHQAKDCIDSFVTHCVRP----FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLAPSS----SNITKLOOIGRGLRLAVNDKGERITKEHADFDFVNELVVIVPQVEGDFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *MFKTMVAFDMDGKVRKPKFELDSEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 AIQQEISEHSLIKQVFSAEELEKSGMVKKGYYGVLFETLEGLGFGEKTDDENFKLTLNQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720
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                                                                                                                                                       GDHPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: $48244
A;Recession: $48244
A;Rolecule type: DAA
A;Residues: 1-1089 <AEF>
A;Fevello, T
B;Buyello, T
B;Buyello, T
B;Buyello, T
B;Buyello, T
B;Buyello, T
B;Buyello, T
B;Buyello, T
B;Buyello, T
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                                            --LIAFTKKETSAVAEAQKLMV-
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nuclear/mitotic apparatus protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T30336
R;Merdes, A.; Ramyar, K.; Vechio, J.D.; Cleveland, D.W.
Cell 87, 447-458, 1996
A;Title: A complex of NuMA and cytoplasmic dynein is essential for mitotic spindle assemt
A;Reference number: Z20828; MUID:97053784; PMID:8898198
A;Accession: T30336
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                          Introns: 15/2; 65/2; 134/1; 190/1; 261/3; 298/1; 374/2; 417/3; 472/2; 512/1; 661/3; 71: Superfamily: HsC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----DITKGDHPIMMGFEPLVNQRLLPPTFPR----YAKIIKREEMVNY-----FAR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 ELYEKSALADFILELSFVSLDFTFEIYWOLOORVDHCAVDDLPYAIRCONLOOKMIDEHE 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FKMANSVTDLRVTG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 GTHLMQDMVKDA----LRSFVDPPVLSPKCYLYNNHQAKDCI-DSFVTHCVRP---FCS 434
                      A;Molecule type: DNA
A;Residues: 1-1607 <WIL>
A;Cross-references: EMBL:Z69660; PIDN:CAA93489.1; GSPDB:GN00028; CESP:F39B1.1
                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DDA
A;Residues: 1-1607 < MT2>
A;Cross_references: EMBL:Z69903; PIDN:CAA93776.1; GSPDB:GN00028; CESP:F39B1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           584 PLQIITKPKVEVLSKMDFLQI----MLNSVHSIPEHWQSQYSEFYMSLDLYHGTQVLDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :: : : | :: | :: | :: | .: | .: | 465 IBSWNLMKSQVKYSTVVDKEDVEN-TLGHLASEMSQYEIAFNDGSTLKLSSSSQRVKQVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 ML------KDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FFPRIPLDLYAK-FKRLNLCQYPRETRIVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 LIQ-----KLGHILEEFATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LSGFELEL--YSMHEYYYIYWYLSEFLYAWLMSTLSRADGSQMAEERIMEEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 LIDRIKTVCEVVNLTNLHCILDFFCE-----FSEQSPCVLSRSLLQTTFLVDNKKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    739 GPY---PYIKDARDPILIMSF---KIWDTELYFPNVVIDMQCIPQDFATLDIETQEYLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---QHLACLGTWVLYHNLRIMIQYL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2%; Score 122.5; DB 2; Best Local Similarity 19.4%; Pred. No. 1.5; Matches 105; Conservative 83; Mismatches 177;
Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 VLIAFTKKETSAVAEAOKLMVQAADLLSAIHN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 QDEFMIFYFNRAEKVDAALHIMLLKQEPQR--
                                                                                                                        R;Thomas, K.
submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 LKICDIAREKVNKAAVFEEEDFQSMTYG
                                                                                                                                                                                                                                                                                            A, Experimental source: clone F46F2
C, Genetics
                                                                                               A; Experimental source: clone F39B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 SNKVPKTIKNDH-
                                                                                                                                                                A;Reference number: Z19545
A;Accession: T22312
                                                                                                                                                                                                                                                                                                                                                                A, Gene: CESP: F39B1.1
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A; Introns: 15/2; 6
C; Superfamily: HSC
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                                                                                                                                                                                            A;Cross-references: EMBL:U40933; NID:g1072142; PID:g1072145; PIDN:AAA81674.1; CESP:F20D1
                                                                                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 DDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFS-RVKFTRVLLTVLIAFTKKETSAVAE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PSFFAFQKCTVSESTINFVNLLRDNVKAAFACEDEGARAKLALT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 RORDKIGHILEEFATLQDEFMTFYFNRAEKVDAALHTMLLKQEPQRQHLACLGTWVLY-- 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHDKLFG-LFEAMSAIEMMDPKMDAGMIGNQVNRKVLN-FEQAI----KDGT-IKIKDLTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 EDOKMINETLSAMNMIGQLPERLDAWKI-----VILNVFCEAIVASRDGVDVXIVDNPT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PELIGIMDICFCCLITWLEGHSLAQIVFTCLYIHNPDFIEDPAMKAFALGILKICDIARE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD------KIIDVAKV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 KVNKAAVF------EEEDFQSMTYGFKMANSVTDLRVTGMLKDV-----E 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F39B1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Loct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T21982; T22312
R;Lightning, J: BML Data Library, February 1996
Submitted to the BML Data Library, February 1996
A;Reference number: 219497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GIQAQNDTTKGDH
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                    3.2%; Score 123.5; DB 2; Length 778; Local Similarity 18.9%; Pred. No. 0.45; Los 115; Conservative 89; Mismatches 188; Indels 215;
                                                                                                                                                                                                                                                                   A,Introns: 98/3; 284/2; 465/2; 735/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F20D12.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 PIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLIDRIKT--VCE---
     R,Wu, X.
submitted to the EMBL Data Library, November 1995
A,Description: The sequence of C. elegans cosmid F20D12.
A,Reference number: Z18462
                                                                                                                                                                                                                                                                                                                                                                                                                                      GWELSMPEK---MEKSNTNW----VDITQDFEEACRELKL
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                                                                                               A;Accession: T16111
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-778 <WUX>
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                                                                                                                                                                                                                                                                                       27;
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                                 A,Residues: 1-2253 <MER>
A,Cross-references: EMBL:Y07624; NID:g1514670; PIDN:CAA68905.1; PID:g1514671
C,Genetics:
A,Gene: NuMA
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                                                                                                                                                                                                                                                                                                                                                     136 HNPDFIEDPAMKAFALGILKICDIAREKV----NKAAVFEEEDFQSMTYGFKMANSVTDL
                                                                                                                                                                                                                                                                                                                                                                                                                       1171 HOSKLGESOGLOALIADLEKKCKEOKELICEAONKAAEAKTLASEKASVSERQLEGIQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 IMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEVVNLTNLHCILDFF
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                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                      Query Match 3.2%; Score 122.5; DB 2; Best Local Similarity 18.6%; Pred. No. 2.4; Matches 125; Conservative 104; Mismatches 255;
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A; Molecule type: mRNA
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promoter regio With the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C04F6.
A;Reference number: Z18346
A;Accession: T15409
A;Accession: T15409
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Reference: EMBL, DDBJ, EVAYT', 188-390, 'TL', 393-613, 'N', 615-688, 'F', 690-71572, 'KEAR', 1577-1603 <NHA>
A;Reference: EMBL, U22335, NID: 91125760; PID: 91125763; PIDN: AAA83587.1; CESP;Vit-5
C;Comment: In Caenorhabditis, vitellogenins are synthesized by 32 cells building the interence of the synthesized by 32 cells building the interestion of the gonad. Vitellogenin 5 undergoes little if any processing before be A;Cross-references: GB:X03044; NID:g6919; PIDN:CAA26849.1; PID:g6920
A;Note: the authors translated the codon TTT for residue 1318 as Thr
R;Spieth, J: Blumenthal, T.
Mol. Cell. Biol. 5, 2455-2501, 1985
A;Title: The Caenorhabditis elegans vitellogenin gene family includes a gene encoding A;Reference number: A33067; MUID:86284606; PMID:3841791 803 749 913 483 914 ---KKNTL-EITHKFVVPENKKTTVSVHTRPVAFIRVPKNODSEÝVEAEEKTISHSOYOM 969 484 LKQEPQRQHLACLGTWVLYHNLRIMIQ-YLLSGFELELYSMHEYYYIYWYLS----EFL 537 637 A,Gene: CESP:vit-5 A;Introns: 288/3; 383/3; 1396/2; 1472/3; 1518/1 C;Superfamily: vitellogenin C;Keywords: egg yolk; glycoprotein; intestine; oocyte F;1-15/Domain: signal sequence #status predicted <51G> F;16-1603/Product: vitellogenin vit-5 #status predicted <MAT> F;602,812,1052/Binding site: carbohydrate (Asn) (covalent) #status predicted Д, A; Molecule type: DNA
A; Residues: 1-99 cSPI2>
A; Residues: 1-99 cSPI2>
A; Cross-references: GB: M11497
A; Cross-references: GB: M11497
Nucleic Acids Res. 13, 5283-5295, 1985.; Cane, J.; Blumenthal, T.
Nucleic Acids Res. 13, 5283-5295, 1985
A; Title: The C. elegans vitellogenin genes: short sequence repeats in the JA; Reference number: A93576; MUID: 85269643; PMID: 4022780
A; Accession: B93576 234 FSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGD ---KMNIRPRVQQ----TDSQNAHAVFYLRYKEMDYIVLPIDMETIDTLVEKYVRNGEFDI 804 KSLLTFLTNDSKFELHRAL-FFYEAERRIPTTIGMPLTISGKMPTILSINGKVSIELEKL GTHLMQDMVKDALRSFV-DPPVLSPKCYLYNNHQAKDCIDSFVTHCVRPFCSLIQIHGHN -YFNRAEKVDAALHTML STEEIDROYET------FGLRINAQGNVLSQWTLPMVLMTEQDFEYTLENKNRPVEFT ----EKLSLYGKQSDELRS--RRVQSGIQMLQEIVK--538 YAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREITMSQAYQNMCA--Gaps Indels 143; ---WNLTN-----LHCILDFFCEFSEQSPCVLSRSLL----QTTFLVDNKKV-Length 1603 294 HPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLID--RIKTVCE------GMFKTMVAFDMDGKVRKPKFELDSEQVRYEHRFAPFNSVMT-234; DB 1; 3.2%; Score 121.5; E 19.9%; Pred. No. 1.8; 91; Mismatches 443 RARQRDKLGHILEEFATLQDEFMTF---706 FSQQNFEQVILKTL-----Best Local Similarity 19.9 Matches 116; Conservative A;Molecule type: DNA A;Reaidues: 1-71 <SPT3> A;Cross-references: GB:X02755 R;Nhan, M. 750 Query Match 342 384 970 296 g g à 셤 ò d ð ₽ g g qq ò ö ð ð

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OY 515 GFELELYSMHEYYYIYWYLSEFLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKK 574		A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Rolesule (1929 < 470> A;Residues: 1-10.29 < 450> A;Cross-references: GB:AE002093; NID:g3402679; PIDN:AAC28982.1; GSPDB:GN00139 C;Genetics: 1-10.29 < 420 C;Genetics: 104/3; 147/2; 205/2; 232/3; 330/3; 336/3; 430/3; 514/3; 587/3; 644/3; A;Matrons: 72/3; 104/3; 147/2; 205/2; 232/3; 330/3; 336/3; 430/3; 514/3; 587/3; 644/3; Query Match Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1029; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1029; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1029; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; Best Local Similarity 18.3%; Pred. No. 1.6; DB 2; Length 1039; DB 202
Db 1082 LEAPQQMYMNTELRTVCDKWIRMCKVEMDARRSPMEHENKEWTLRTELLAARPQMP 1137 Qy 638 PPVHYLQFKEMSDLNFYSPPPQSPELYVAASKHFQQAKMILENIPNPDHE 687 1138 SSLRQLREQPHREVQLAFNARWGSSKKSEITVNAQLEGSTEQKKFIRNIEREYKGIPEYE 1197 Qy 688 VNRILKVAKPNFVVMKLLAGGHKKESKVPPEPDFSAHKXFPVVK 731 1198 L-LIKAARLNQVNVVSEYKLTPQSBYTFSRIFDLIK 1232	KIAA0729 procein - human (fragment) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) Rivagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.; Tanaka, A.; Kotani, H Rivagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.; Tanaka, A.; Kotani, H Rivagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Misominary; Translated from GB/EMBL/DDBJ A; Reference mumber: Z17595; MUD199087487; PMID19872452 A; Residues: 1-1196 cNAG- A; Residues: 1-1196 cNAG- A; Residues: Lishikamana source: Brain R; Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. A; Reference number: Z16471 A; Reference number: Z16471 A; Residues: Z79-1196 cWAM- A; Cross-references: EMBL:AL050092 A; Residues: Z79-1196 cWAM- A; Residue	Query Match 3.1%; Score 119; DB 2; Length 1196; Best Local Similarity 19.3%; Pred, No. 1.8; Matches 124; Conservative 99; Mismatches 235; Indels 186; Gaps 31; Oy 97 INDITIEDED TO THE STATE

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Gaps

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| | : :|: |: ||: 1|GESLVEDKLSLINSNWIAVTSRAEEWINIJMEYQKHMEAFDQKVANVTTWIYRAEILLD 1705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 MIGNOVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCLITWLEGHSLAQTVFTCL 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----QDFEEACRELKLGEL--LHDKLFGLFEAMSAIEMM----------DPKMDAG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : : | : : : : | : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : | : : : : | : : : : | : : : : : | : : : : | : : : : : | : : : : | : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : | : : : : : | : : : : : | : : : : | : : : : : | : : : : | : : : : | : : : : | : : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GFKMANSVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 RVLLTVLIAFTKKETSAV--AEAQKLMVQAADL-----LSAIHNSLHHGIQAQNDTTKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFMTFYFNRAEKVDAALHTMLLKQEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELELYS
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                                                                                                                                                                                                                                                                                                                                                                       Length 3660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----BDTTFVMTESMTVBTTYVPSTYLAEILQLLQALSEVEERLNS
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         homology homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       229;
                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                              Score 117.5;
Pred. No. 11;
    spectrin/dystrophin repeat
spectrin/dystrophin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFAPFNSVMTPPPVHYLOFKEMSDLNK 653
                                     F;2930-3037/Domain: spectrin/dystrophin reper
F;3038-3075/Region: hinge
F;3052-3089/Domain: WW repeat homology <WWI>
F;3079-3357/Region: cysteine-rich
F;3481-3502/Region: leucine zipper motif
F;3547-3568/Region: leucine zipper motif
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-----CEMKS 2117

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model - protein search, OM protein Run on:

August 10, 2004, 21:47:26; Search time 13 Seconds (without alignments) 2935.956 Million cell updates/sec

Title: Perfect score:

US-10-001-857-145 3849 1 MVWKASVDDDDSGWELSMPE......KVPPEFDFSAHKYFPVVKLV Sequence:

733

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q02197 saccharomyc	9 homo	Q9upw6 homo sapien	mus m	m	a	P18947 caenorhabdi	Q9xhr2 zea mays (m		P11533 gallus gall		P98197 mus musculu	7		_	Н				P08032 mus musculu		m			Q9pqb4 ureaplasma		026640 methanobact		O33600 sulfolobus		0 arabi	homo	Q9bpx3 homo sapien
SUMMARIES	ID	MK10 YEAST	SPCA HUMAN	SAB2 HUMAN	SAB2 MOUSE	NMD2 YEAST	VIT3_CAEEL	VIT4_CAEEL	IF3A MAIZE	VITS CAEEL	DMD CHICK	BAC1 HUMAN	Alla MOUSE	YIO9 YEAST	SPOF_SCHPO	TEL1_YEAST	TRA1 YEAST	IKAP HUMAN	DOR1_YEAST	EG52_XENLA	SPCA MOUSE	M12_STRPY	KL61_DROME	HS90_BRUPA	RHG8_HUMAN	DPO3_UREPA	GCN1_YEAST			RASO SULAC				CND3_HUMAN
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EMBL; M94533; AAA34749.1; -.
EMBL; U18779; AAB64989.1; -.
PIR, S31288; S31288.
Germonline; 139057; -.
SGD; S0000779; MAK10.
GO; GO:0004042; F:amino-acid N-acetyltransferase activity; IDA.
GO; GO:0006474; P:N-terminal protein amino acid acetylation; IDA.

008739 mus musculu Q24167 drosophila	P07901 mus musculu P12753 saccharomyc	Q8nf91 homo sapien	P36114 saccharomyc	Q01432 homo sapien	P40164 saccharomyc	O14248 schizosacch	P98196 homo sapien	Q07518 plantago as	Q9jhu4 mus musculu
AMD3_MOUSE SIMA_DROME	HS9A_MOUSE RA50_YEAST	SNE1_HUMAN	YKZ8_YEAST	AMD3_HUMAN	YNU1 YEAST	YE62 SCHPO	A11A HUMAN	RRPO_P1AMV	DYHC_MOUSE
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105.5	105	105	104.5	104.5	104.5	104.5	104.5	104.5	104.5
34 35	36	38	39	40	41	42	43	44	45

ALIGNMENTS

	(°)	ina; Saccharomycetes; haromyces.	SEQUENCE FROM N.A. MEDINE-93012936; PubMed=1398065; Lee YJ., Wickner R.B.; Lee YJ., Wickner R.B.; WAKIO, a glucose-repressible gene necessary for replication of a dsRNA virus of Saccharomyces cerevisiae, has T cell receptor alpha-subunit motifs." Genetics 132:87-96(1992).	, Yelton M.A., Allen E.,		Nature 387:78-81(1997). -!- FUNCTION: Has a role in the propagation of L-A and M viruses, perhaps in the viral assembly. It is apparently directly needed for optimum respiration. -!- INDUCTION: Glucose-repressed. -!- SIMILARITY: SOME, TO T-CELL RECEPTOR ALPHA SUBUNIT VARIABLE REGIONS.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRT;	Created) Last sequence update) Last annotation update) otein MAK10.	ker's ye i, Sacche iycetacea	18065; e gene r i cerevie	59868; , Hennes	n M., Gu Kayser Ca K., No D., Sehl Botster Sacchard	the propsembly.	is copyright. titute of Bio atics Institut nstitutions arement is not of the series agreement consequence.
STANDARD;	26, Creat 26, Last 42, Last le proteir	MAXIO OR YEL053C. Saccharomyces cerevisiae (Baker's yeast). Saccharyota, Fungi, Ascomycota, Saccharomycotina, Sacch Saccharomycetales, Saccharomycetaceae, Saccharomyces.	11) SEQUENCE FROM N.A. MEDLINE-93012936; PubMed=1398065; Lee YJ., Wickner R.B.; "MAKI0, a glucose-repressible gene necessary deRNA virus of Saccharomyces cerevisiae, has alpha-subunit motifs."; Genetics 132:87-96(1992).	12) SECUENCE FROM N.A. STRAIN=S288C / AB972; MEDLINE=97313264; PubMed=9169868; Dietrich F.S., Mulligan J.T., Hennessy K.M.,	Cherry J.M., Avites E., Delina M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., C Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogre Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.; "The nucleotide sequence of Saccharomyces cerevisiae chron	Nature 387:78-81(1997). -!- FUNCTION: Has a role in the 1 perhaps in the viral assemble for optimum respiration. -!- INDUCTION: Glucose repressed -!- SIMILARITY: SOME, TO T-CELL 1 REGIONS.	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinfor the European Bioinformatics Institute. use by non-profit institutions as lon modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
T 1 YEAST MKIQ YEAST	00219/; 01-JUL-1993 01-JUL-1993 10-OCT-2003 Glucose repr	MAK10 OR YEL053C. Saccharomyces cer Eukaryota; Fungi; Saccharomycetales NCBI_TAXID=4932;	111 SEQUENCE FROM N.A. MEDLINE=93012936; PubMe Lee YJ., Wickner R.B. "MAKIO, a glucose-repre dsRNA virus of Saccharo alpha-subunit motifs."; Genetics 132:87-96(1992	SEQUENCE FROM N.A STRAIN=S288c / AB: MEDLINE=97313264; Dietrich F.S., Multiple A.	Ataulo K., A Cherry J.M., Hunicke-Smit Lin D., Mose Oh C., Petel Smith V., Ta	Nature 387:7 -!- FUNCTION perhaps for opti -!- INDUCTIC -!- SIMILARI	This SWISS-I between the the Europear use by nor modified and entities rec or send an e
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V-----AYDPPLASVAAIADRLLRCVISWLNDYQTLPTTVLSCRYTESLLSSLVKGTTA
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Catarrhini, Hominidae, Homo.
                                                                                                                       155;
                                                                                Length 733;
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21-JUL-1986 (Rel. 01, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Spectrin alpha chain, erythrocyte (Erythroid alpha-spectrin)
SPTAI OR SPTA.
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                                         11148C1FC6BB0931 CRC64;
                                                                          7.0%; Score 270.5; DB 1;
ilarity 19.7%; Pred. No. 4.1e-12;
Conservative 121; Mismatches 270;
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                                       84302 MW;
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Mammalia; Eutheria; Primates;
  InterPro; IPR007244; Mak10.
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                    Pfam; PF04112; Mak10;
SEQUENCE 733 AA; 8-
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Les 134; Conserv
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Speicher D.W., Davis G., Yurchenco P.D., Marchesi V.T.; "Structure of human erythrocyte spectrin. I. Isolation of the alpha-I domain and its cyanogen bromide peptides."; J. Biol. Chem. 258:14931-14937(1983).
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                                                                                                                                                                                                                                                                                                                                                  Sahr K.E., Tobe T., Scarpa A., Laughinghouse K., Marchesi S.L.,
Agre P., Linnenbach A.J., Marchesi V.T., Forget B.G.;
"Sequence and exon-intron organization of the DNA encoding the alpha
I domain of human spectrin. Application to the study of mutations
causing hereditary elliptocytosis.";
J. Clin. Invest. 84:1243-1252(1989).
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For human erythrocyte
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Blood 84:303-308(1994).
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Parquet N., Devaux I., Boulanger L., Galand C., Boivin P.,
Lecomte M.-C., Dhermy D., Garbarz M.;
"Identification of three novel spectrin alpha I/74 mutations in
       Scarpa A.L., Coupal E., Leto 'Speicher D.W., Marchesi V.T.,
                                                                                                             sequences of human erythroid
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MEDLINE=86205962; PubMed=3458204;
Linnenbach A.J., Speicher D.W., Marchesi V.T., Forget
"Cloning of a portion of the chromosomal gene for hun
alpha-spectrin by using a synthetic gene fragment.";
Proc. Natl. Acad. Sci. U.S.A. 83:2397-2401(1986).
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MEDILINE=97001215, PubMed=8844207,
MAILIGLE P., Alloisio N., Morle L., Delaunay J.;
"Spectrin mutations in hereditary elliptocytosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS EL2 CYS-28; HIS-28; LEU-28 AND SER-28.
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Unpublished observations (MAR-1995)
Sahr K.E., Laurila P., Kotula L., S
Linnenbach A.J., Winkelmann J.C., S
Curtis P.J., Forget B.G.;
"The complete cDNA and polypeptide
                                                                                                                                                                              Biol. Chem. 265:4434-4443 (1990)
                                                                                                                                                                                                                                                                                    PRO-471.
MEDLINE=90009318; PubMed=2794061;
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MEDLINE=84087888; PubMed=6654896;
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VARIANT EL2
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with partial skipping of exon 46.";
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Zarkowsky H.S., Baruchel A., Ballas S.K., Dhermy D., Palek J.,
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MEDINE=9943025, Pubmed=8226774;
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MEDLINE=93253053; PubMed=8486776;
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                                                                                                                                    Blood 78:1364-1372(1991).
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Gallanello R.;
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                                                          Forget B.G.;
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1888 VLHEES-----QNKEISSKIEALNEKTPSLAKAIAAWKLQLEDDYAFQEFNWKADVV 1939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1780 D-KAAVGQE---EIQLRLAQFVEHWEKLKELAKARGLKLEESLEYLQFMQNAEEEEAWIN 1835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 RLLPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEVVNLTNLHCILDF-FCEFSEQSPCV 365
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-!- FUNCTION: Spectrin is the major constituent of the cytoskeletal network underlying the erythrocyte plasma membrane. It associates with band 4.1 and actin to form the cytoskeletal superstructure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 --EEEDF-----DSMTYGFKMANSVTDL----RVTGMLKDVED-----DMQRRVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the erythrocyte plasma membrane.
-!- SUBUNIT: Composed of nonhomologous chains, alpha and beta, which aggregate side-to-side in an antiparallel fashion to form dimers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDILTNE=84550920; PubMed=8193371;
Perrotta S., del Giudice E.M., Alloisio N., Sciarratta G., Pinto L.,
Delaunay J., Cutillo S., Lolascon A.;
"Mild elliptocytosia associated with the alpha 34 Arg-->Trp mutation
in spectrin Genova (alpha 1/74).";
Blood 83:3346-3349(1994)
                                                                                                                                                                                                                                                                                                                                                                                         is due
                                            from
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DISEASE: Defects in SPTA1 are a cause of rhesus-unlinked elliptocytosis 2 (EL2) [MIM:130600, 182860, 166900].
Elliptocytosis (also known as ovalocytosis) is a genetically heterogeneous, autosomal dominant hematologic disorder. It is
                                                                                                                                                                                                                                                    MEDLINE-89323436; PubMed-2568861;
Morle L., Morle F., Roux A.F., Godet J., Forget B.G., Denoroy L., Garbarz M., Dhermy D., Kastally R., Delaunay J.;
"Spectrin Tunis (Sp alpha 1/78), an elliptocytogenic variant, is to the CGG-->TGG codon change (Arg-->TRp) at position 35 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95290423; PubMed=7772539;
Perrotta S., Iolascon A., de Angelis F., Pagano L., Colonna G., Cutillo S., del Giudice E.M.;
Cutillo S., del Giudice E.M.;
"Spectrin Anastasia (alpha 1778): a new spectrin variant (alpha Arg-->Thr) with moderate elliptocytogenic potential.";
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Matches 175; Conservative 142; Mismatches 307; Indels 280;
    spectrin variant that is carries a mutation distant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 134; DB 1; Length 2418;
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"Spectrin Jendouba: an alpha II/31 associated with elliptocytosis and the dimer self-association site."; Blood 80:809-815(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT EL2 ANASTASIA THR-45.
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Blood 74:828-832(1989).
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                                                                                                               QHNQSKAİEERYAALLKRWEQLLEASAVHRQK-----LLEKQLPLQKAEDLFVEFAHK 2050
                                                                                                                                                                                                                                   530
----MODMVKDALRSFVD----PPVLSPKCYLYN- 413
                                                                                                                                                                            2051 ASALNNWCERMEBNLSEPVHCVSLNEIRQLQKDHEDFLASLARAQADFKCLLELDQQIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYVSLEDY--TAFLIDKESENIKSSDEIENAFQALAEGKSYITK----EDMKQALTPEQV
                                  1940 EAWIADKETSLKTNGN--GADLGDFLTLLAKQDTLDASLQSFQQERLPEITDLKDKLISA
                                                                         414 NHQAKDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQ---DEFMTFYF-
                                                                                                                                                                                                                                   --LSGFEL-ELYSMHEYYYIY
                                                                                                                                                                                                                                                                    LGVPSSPYTWITVEVLERTWKHLSDIIEEREQELQKEEARQVKNFEMCQEFEQNASTFLQ
                                                                                                                                                                                                                                                                                                            WYLSEFLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREIT----
                                                                                                                                                                                                                                                                                                                                               2171 WILETRAYF-----LDGSLLKETGTLESQLEANK----RKOKEIQAMKRQLTKIVDL
                                                                                                                                                                                                                                                                                                                                                                                     ----MSQAYQ---NMCAGMFKTMVAFDMDGKVRKPKFELDSE
                                                                                                                                                                                                                                                                                                                                                                                                                            2219 GDNLEDALILDIKYSTIGLAQOWDQLYQLGLRMQHNLEQQIQAKDIKGVSEETLKEFST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                664 -YVAASKHFQQAKMI---LENIPNPDHEVNRILKVAKPNFVVMKLLAGGHKKESKVPPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=93937452; PubMed=10470851;
Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N.,
Kikuno R., Kotani H., Ishikawa N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIV
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:197-205(1999).
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
DNA-binding protein SATB2 (Special AT-rich sequence-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FitzParrick D.R., Carrier T.M., McCaren L., Leek J.P., Wightman P., Williamson K., Gautier P., McGill N., Hayward C., Firth H., Markham A.F., Farthes J.A., Bonthron D.T.,

"Identification of SATHES as the cleft palate gene on 2q32-q33.";

Hum. Mol. Genet. 12:2491-2501(2003).

-! FUNCTION: May play an important role in palate formation.

-! SUBCELPLULAR LOCATION: Nuclear (By similarity).

-! TISSUE SPECIFICITY: High expression in adult brain, moderate expression in fetal brain, and weak expression in adult liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaran Jaraman, Mandara, Craniata, Vertebrata, Buteleostomi,
Bukaralia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVRYEHRFAPFNSVMTPPPVHYLQFKE-MSDLNKYSPPPQSPEL
                                                                                                                                                        ----NRAEKVDAAL----HIMLLKQ--EPQRQH-
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                                                                                                                                                                                                                                 LG-----TWVLYHNLRIMIQYL------
LSRSLLQTTFLVDNKKVFGTHL----
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MEDLINE=22855719; PubMed=12915443;
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration
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kidney, and spinal cord and in select brain regions, including amygdale, corpus callosun, candate nucleus, and hippocampus. DISEASE: Involved in isolated cleft palate through 2 chromosomal translocations t(2;7) and t(2;11).
SIMILARITY: Belongs to the CUT homeobox family.
SIMILARITY: Contains 2 CUT domains.
SIMILARITY: Contains 1 homeobox domain.
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PROSITE; PS00027; HOMEOBOX 1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Nuclear protein; Repeat;
Chromosomal translocation.
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20.9%; Pred. No. 0
ive 91; Mismatch
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Genew; HGNC:21637; SATB2.
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InterPro; IPR003350; Hmoeo.CUT.
InterPro; IPR001356; Homeobox.
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Pfam; PF00046; homeobox; 1.
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Matches 132; Conserv
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Note-No experimental confirmation available;

Note-No Expression first detected at 10.5 dpc in the maxillary component of the first pharyngeal arch and the lateral aspect of the frontonasal process in the regions that will subsequently fuse to form the primary palate. At 11 - 11.5 dpc, the expression pattern demarcates the region of the medial aspect of the maxillary process within the primitive oral cavity, which will form the palate shelf. By 12.5 dpc, symmetrical expression is seen in the medial edges of the developing palate shelves and this continues until 13.5 dpc when the strongest expression is in the mesenchyme underlying the medial edge epithelia. By the time of palatal shelf fusion at 14.5 dpc the expression is dramatically down-regulated. No expression detected elsewhere in the embryo at any stage examined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
525 ENPSPENRTL----WENLC----TIRRF-----LNLPQHERDVIYEEESRHHHSERMQ 569
                         632 NSVMTPP-PVHYLQ-----FKEMSDLNKYSPPPQSPELYVAASKHFQQAKMILENIP-- 682
                                                     570 HVVQLPPEPVQVLHRQQSQPAKESSPPREEAPPPPPPTEDSCAKKPRSRTKISLEALGIL 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORVIZ4;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
DNA-binding protein SATE2 (Special AT-rich sequence-binding protein
                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22855719; PubMed=12915443;
FitzPatrick D.R., Carr I.M., McLaren L., Leek J.P., Wightman P.,
Williamson K., Gautier P., McGill N., Hayward C., Firth H.,
Markham A.F., Fantes J.A., Bonthron D.T.;
"Identification of SATE2 as the cleft palate gene on 2q32-q33.";
Hum. Mol. Genet. 12:2491-2501(2003).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the CUT homeobox family. SIMILARITY: Contains 2 CUT domains. SIMILARITY: Contains 1 homeobox domain.
                                                                               -----NPDHEVNRIL--KVAKPNFVVMK 703
                                                                                                 IsoId=Q8VI24-2; Sequence=VSP_008967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q8VI24-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                             SATB2 OR KIAA1034.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVVQLPPEPVQVLHRQQSQPTKESSPPREEAPPPPPPTEDSCAKKPRSRTKISLEALGIL 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developmental protein; Homeobox; DNA-binding; Nuclear protein; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: | : | : | | : : | | : : EQLDGSLEYDNREEHAEFVLVRKDVLFSQLVETALLALGYSHSSA-AQAQGIIKLGRWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 LPLSYVTDAPDATVADMLQDVYHVVTLKIQLQSCSKLEDLPAEQWNHATVRNALKELLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 VNORLLPPTFPRYAKIIKREEMVNYFA------RLIDRIKTV-CEVVNLTNL--H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 MNOSTLAKECPLSOSMISSIVNSTYYANVSATKCOEFGRWYKKYKKIKVERVERENLSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 CILDFFCEFSEQSPCVLSR----SLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVDPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 IQIHGHNRARQRDKLGHILBEFATLQDEFMTFYFNRAEKVDAALHTMLLKQEPQRQHLAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 LŚPQLSPQLVRQQIAMAHLINQQIAVSRLLAHÖHPQAINQQFLNHPPIPRAVKPEPTNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----FLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 EERDPEVEL----EHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --IMMGFEPL-
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20.9%; Pred. No. 0.14;
Lve 91; Mismatches 227; Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496 LGTWVLYHNLRIMIQYLLSGFELE---LY-----SMHEYYYIYWYLSE--
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733 AA; 82559 MW; 153CFDICC3491F25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 2). /FIId=VSP_008967.
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                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX 1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUT 2.
HOMEOBOX.
                                                                                                                               EMBL; AF319623; AAL37172.1; -.
EMBL; AK129270; BAC38080.1; ALT_INIT.
InterPro; IPR007108; Cut_homeo.
InterPro; IPR003350; Hmoeo CUT.
InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                Pfam; PF02376; CUT; 2.
Pfam; PF00046; homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Ribes L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Involved in nonsense-mediated decay of mRNAs containing premature stop codons. It interacts, via its C-terminus, with NAM7/UPF1. Could be involved in determining the efficiency of translational termination or reinitiation or factors involved in the initial assembly of an initiation- and termination-competent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee S.I., Umen J.G., Varmus H.E.;
"A genetic soreen identifies cellular factors involved in retroviral
- I frameshifting.";
Proc. Natl. Acad. Sci. U.S.A. 92:6587-6591(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              required for
                                                                                                                                                                                                                                                                                                                                                                                                     He F., Jacobson A.; "Identification of a novel component of the nonsense-mediated mRNA decay pathway by use of an interacting protein screen."; Genes Dev. 9:437-454 (1995).
                                                                       01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Nonsense-mediated mRNA decay protein 2 (Up-frameshift suppressor
NMD2 OR UPF2 OR IFSI OR SUAI OR YHR077C.
                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95189082; PubMed=7883167;
Cui Y., Hagan K.W., Zhang S., Peltz S.W.;
Tidentification and characterization of genes that are requithe accelerated degradation of mRNAs containing a premature translational termination codon.";
Genes Dev. 9:423-436(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                         1089 AA
                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=95327692; Pubmed=7604038;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=95189083; PubMed=7883168;
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Germonline, 133934, --
SGD: S0001119; NMD2.
GO: GO:0005844; C:polysome; IDA.
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EMBL, U12137; AAA66521.1; -.
EMBL, U28158; AAA74948.1; -.
EMBL, U10556; AAB68893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 265:2077-2082(1994).
                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                    YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 AITLGEFFKLEIPELEGASNDDL-----KETA-----SPMITNQILPPN--- 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 AKIIKREEMVNYFARLIDRIKTVCEV-------VNLTNLHCILDFFCEFSEQSPCVL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 QRLWENEDTRKFYEILPDISKTVEESQSSKTEKDSNVNSKNINL---FFTDL-EMADC-- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 SRSLLQTTFLVD--NKKVFGTHLMQDMVKD-ALRSFVDP-----PVLSPKCYLYNNHQA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KDIIDDLSNRYWSSYLDNKATRNRIJKFFMETQDWSKLPVYS-RFIATNSKYM 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 KDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRNTGFIKKLKKGFVKGSESSLLKDLSEASLEKYLSEIIVTVTECLLNVLNKNDDVIAAV 94
                                                                                                                                                                                                                                                                                                                      24 KSNTNWV------HDKLFGLF
                                                                                                                                                                                                                                                                                                                                                                                                                   EAMSAI - EMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --NKINVKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 YAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREITMSQAYQNMCAGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 LKDVEDDMORRVKSTRSROGEERDPEVELEHQOCLAVFSRVKFTRVLLITVLIAFTKKETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 ALHTMLLKQEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFL
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                                                                                                                                                                                                                                                                   222;
                                                                                                                                                                                                                                                                                                                                                                                                                                            | :| : : : : : | | | | :: :: | | | | ELISGLHQRFRGRFTSPLLG----AFLQAFENPSVDIES-ERDEL----
                                                                                                                                                                                                                   Query Match 3.3%; Score 127; DB 1; Length 1089; Best Local Similarity 17.6%; Pred. No. 0.24; Matches 117; Conservative 124; Mismatches 202; Indels 22
                                                                                                                         ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                                                                                                  2 2 D -> YQQ (IN REF. 3 AND 4).
1089 AA; 126746 MW; 13BBE725675CBF52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 HKKV-NKLQREHQKCQIRTGKLRDEYVE-EYDKLLDFIRFK-
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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InterPro; IPR003890; IF eIF4G.
InterPro; IPR001193; UDF2.
Pfam; PF02884; MIF4G; 3.
Pfam; PF040S0; Upf2; 1.
                                                                                               SMART; SM00543; MIF4G; 3. DOMAIN 843 975
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VIT-3 OR F59D8.1.
Caenorhabditis elegans.
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                                                                                                                                                                      SEQUENCE
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                                                                                                                                                  CONFLICT
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CONFLICT
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KMNIRPRVQQ----TDSQNAHAVFYLRYKEMDYIVLPID-METIDNVVEKYVRNGEFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LTN-----LHCILDFFCEFSEQSPCVLSRSLL----OTTFLVDNKKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  803 IKSLLTFLTNDSKFELHRAL-FFYEAERRIPTTIGMPLTISGKMPTLLSINGKVSIELEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 IHGHNRARQRDKLGHILEEFATLQDEFMTF------YFNRAEKVDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        913 L-----KKNTL-EITHKFVVPENKKTTVSVHTRPVAFIRVPKNQDSEYVETEEKTISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 LHTMLLKQEPQRQHLACLGTWVLYHNLRIMIQ-YLLSGFELELYSMHEYYYIYWYLS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --EFLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREITMSQAYQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 FSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 HPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEVVN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              862 LGARLVLDIVPTVATTHVTEMRFWYPVI------EQGVKSLQSARLHTPLRFESTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89; Mismatches 234; Indels 145; Gaps
                                                                                                                                                                                         sources of
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1603;
                                                                                                                                 Waterston R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Precursor of the egg-yolk proteins that are nutrients during embryonic development (Potential).
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Contains 1 VWFD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCA0276E477D37DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 125.5; Di
20.0%; Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VITELLOGENIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PP00094; vwd; 1.
MarkT; Sw00638; LPD N; 1.
SWART; Sw00216; vwD; 1.
Storage protein; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR001747; Lipid transprt_N.
InterPro, IPR001846; VWF D.
Pfam; PF01347; Vitellogenin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1603 AA; 186529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC024137; AAK09075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormPep; F59D8.1; CE20900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                     Rhabdraidae, Pelo
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1308
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1137 PSSLRQLREQPHREVQLALNAKWGSSKKSEITFNAQLEQSTEQKKFLRNIEREYKGIPEY 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter regions and honology to the vertebrate genes.";
Nucleic Acids Res. 13:5283-5295(1985).
-!- FUNCTION: Precursor of the egg-yolk proteins that are sources of nutrients during embryonic development (Potential).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Synthesized in Caenorhabditis only by 32 cell building the intestine of adult hermaphroditic individuals; they are cotranslationally secreted into the body cavity and subsequently taken up by the gonad.
-!- SIMILARITY: Contains 1 VWFD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spieth J., Denison K., Kirtland S., Cane J., Blumenthal T.; "The C. elegans vitellogenin genes: short sequence repeats in the
                                                                                                         MW; E303170325BC99BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blumenthal T., Spieth J., Zucker E.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases
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L. S. V. (IN REF. 2).

EVAYT -> RSRLH (IN REF. 2).

T. S. (IN REF. 2).
                                                                  687 EVNRILKVAKPNFVVMKLLAGGHKKESKVPPEFDFSAHKYFPVVK
                                                                                                                                                                                                                                                                                           VIT4_CAEEL STANDARD; PRT; 1603 AA. P18947; Q9BPB3; 01-NOV-1990 (Rel. 16, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
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VITELLOGENIN 4.
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SIGNAL 15 POTENTIAL.
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Wormbep; F55DB 2; CES6817.

InterPro; IPR00174; Lipid transprt_N.

InterPro; IPR001846; WWF D.

Pfam; PF01347; Vitellogenin_N; 1.

SMART; SM00638; LPD N; 1.

SMART; SM00216; VWD; 1.
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MEDLINE=85269643; PubMed=4022780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC024137; AAK09074.1; -.
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275 275
1603 AA; 186307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vitellogenin 4 precursor.
VIT-4 OR F59D8.2.
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1455
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1076
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                                                                                                                                                                                                                                                                            437
                                                                                                     749
                                                                                                                                       344
                                                                                                                                                                                                                                                                                                              912
                                                                                                                                                           ---KMNIRPRVQQ---TDSQNAHAVFYLRYKEMDYIVLPID-METIDNVVEKYVRNGEFD
                                                                                                                                                                                                                                                                            PGTHLMQDMVKDALRSFVDP----PVLSPKCYLYNNHQAKDCIDSFVTHCVRPFCSLIQ
                                                                     FSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGD
                                                                                                    FSQONFEQVILKTL------EKLSLYGKQSDELRS--RRVQSGIQMLQEIVK--
                                                                                                                                       HPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEVVN-----
                                                                                                                                                                                                                                        803 IKSLLTFLTNDSKFELHRAL-FFYEAERRIPTTIGMPLTISGKMPTILSINGKVSIELEK
                                                                                                                                                                                                                                                                                                            LGARLVLDIVPTVATTHVTEMRFWYPVI------EQGVKSLQSARLHTPLRFESTVE
                                                                                                                                                                                                                                                                                                                                               -YFNRAEKVDAA
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                                                                                                                                                                                                                                                                                                                                                                                                                479 LHTMLLKQEPQRQHLACLGTWVLYHNLRIMIQ-YLLSGFELBLYSMHBYYYIYWYLS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --EFLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKKVRPLSREITMSQAYQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1017 PVEPTARVTIGNLEKTÖLSEIKFDKİFEKEFDLENNESENRRQYFHKMIREİQSEQGFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCA-----GMFKTMVAFDMDGKVRKPKFELDSEQVRYEHRFAPFN-----SVMTPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSSLRÓLREOPHREVOLALNAKWGSSKKSETTFNAOLEOSTEOKKFLRNÍEREYKGIPEY
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sabelli P.A., Burgess S.R., Valasek L., Shewry P.R.; "Molecular cloning and characterisation of a maize cDNA for a homologue of the large subunit of the eukaryotic initiation factor 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Genet. 261:820-830(1999).
-!- FUNCTION: Binds to the 40S ribosome and promotes the binding of methionyl-tRNAi and mRNA.
-!- SUBJUNIT: eIF-3 is composed of at least 12 different subunits (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta)
(Eukaryotic translation initiation factor 3 large subunit) (eIF3a).
TIF3a1 OR IF3a.
Ten anys (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays (Maize).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
PACCAD clade, Panicoideae, Andropogoneae; Zea.
                                                                                                                                                                                                         -----LTN-----LHCILDFFCEFSEQSPCVLSRSLL----QTTFLVDNKKV--
                                   145;
   Length 1603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVNRILKVAKPNFVVMKLLAGGHKKESKVPPEFDFSAHKYFPVVK 731
                                   Indels
Score 125.5; DB 1;
Pred. No. 0.52;
9; Mismatches 234;
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STRAIN=CV. LG11, TISSUE=Root tip;
MEDLINE=99320843; PubMed=10394920;
 3.3%; Sco:
20.0%; Prective 89; 1
                                   Conservative
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                   Similarity
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                                   117;
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Q9XHRZ;
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                                                                                                                                                                                                                                                                                                                                                                          247 LIAFTKKETSAVAEAQKL--MVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGF-EPL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                           VNQRLLPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEVVNLTNLHCILDFFCEFSEQSP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KCY-----LYNNHQAKDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHI--LEB 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 KFLWETYRTVLEILRNNSKLEALYAMTAHRAFQFCKQYKRTTEFRSCVRSIRNHLANLNK 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QMAEERIME-----EQQKGRSSKKTKKKKKVRPLSREITMSQAYQNMCAGMFKTMVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       644 QFKEMSDLNKYSPPPQSPEL---YVAASKH-----FQQAKMILEN----IPNP
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                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                        Indels 169;
                                                                                                                                                                                                                                                                                                          Length 962;
                                                                                                                                                                                                                                                                       436E9B8658921E76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 CVLSRSLLQTTFLVDNKKVFGTHLMQDM-----VKDALRSFV-
                                                                                                                                                                                                                                                                                                       ; Score 121.5; DB 1;
; Pred. No. 0.52;
87; Mismatches 191;
SIMILARITY: Contains 1 PCI domain.
SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
VIT-5 OR C04F6.1
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Pfam; PF01399; PCI; 1.
SMART; SM00088; PINT; 1.
Initial Ector; Protein biosynthesis.
SEQUENCE 962 AA; 111563 MW; 436E9B86
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I woleic Acids Res. 13:5283-5295(1985).

I POWCINION: Precursor of the egg-yolk proteins that are sources of nutrients during embryonic development (Potential).

I SUBCELULAR LOCATION: Secreted.

I SUBCELULAR LOCATION: Secreted.

I TISSUB SPECIFICITY: Synthesized in Caenorhabditis only by 32 cells building the intestine of adult hermaphroditic individuals; they are cotranslationally secreted into the body cavity and subsequently taken up by the gonad.

I PPM: Vitellogenin 5 undergoes little if any processing before being packaged into yolk platelets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                               Spieth J., Blumenthal T.;
"The Caenorhabditis elegans vitellogenin gene family includes a gene encoding a distantly related protein.";
Mol. Cell. Biol. 5:2495-2501(1985).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                         Spieth J., Denison K., Zucker E., Blumenthal T.; "The nucleotide sequence of a nematode vitellogenin gene."; Nucleic Acids Res. 13:7129-7138(1985).
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(IN REF. 3).
(IN REF. 3).
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V -> L (IN REF. 3).
SRRLH -> EVAYI (IN REF. 3).
SI -> TL (IN REF. 3).
H -> N (IN REF. 3).
L -> F (IN REF. 3).
PLL -> RFW (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VITELLOGENIN 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Storage protein; Multigene family; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U42835; AAA83587.1; -.
EMBL, X02755; CAA26532.1; -.
PIR; A03334; VJKW5.
PIR; F89497; F89497.
Normeep; C04F6.1; CE03921.
InterPro; IPR001747; Lipid transprt N.
InterPro; IPR001846; VWF.D.
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=86041902; Pubmed=3855245;
                                                                                          SEQUENCE FROM N.A.
MEDLINE=86284606; PubMed=3841791;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                        3.2%; Score 121.5; DB 1; Length 1603; 19.9%; Pred. No. 1;
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F -> N (IN REF. 3).
E -> K (IN REF. 3).
RQERS -> SKNAR (IN REF. 3).
QSSS -> KRAR (IN REF. 3).
MW; 751A618504E3C55F CRC64;
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"Nucleotide sequence of chicken dystrophin cDNA.";
Nucleic Acids Res. 16:11815-11815(1988).
                                                                                                                                                                                                     Query Match 3.2%; Score 121.5; UB 1;
Best Local Similarity 19.9%; Pred. No. 1;
Matches 116; Conservative 91; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 RARQRDKLGHILEEFATLQDEFMTF-------
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(Rel. 12, Last sequence update)
(Rel. 41, Last annotation update)
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MEDLINE=89098331; Pubmed=3062582;
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                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lemaire C., Heilig R., Mandel J.L.,
"The chicken dystrophin cDNA: striking conservation of the C-terminal
coding and 3' untranslated regions between man and chicken.";
EMBO J. 7:4157-4162(1988).
-!- FUNCTION: May play a role in anchoring the cytoskeleton to the
                                                                                                                             plasma membrane.

SIMILARITY: THE ACTIN-BINDING DOWAIN IS OF A TYPE FOUND IN MA
ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN,
ABP-120, ABP-180, OR BETA-FODRIN).

SIMILARITY: Contains 2 calponin-homology (CH) domains.
SIMILARITY: Contains 22 spectrin repeats.
SIMILARITY: Contains 1 WM domain.
SIMILARITY: Contains 1 WM domain.
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CH 2.
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SPECTRIN 2
SPECTRIN 3
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SPECTRIN 9
SPECTRIN 1
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PIR; S02041; S02041.
HSSP; P46399; BHD.
InterPro; IPR001589; Actbind actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR002017; Spectrin.
                  IISSUE=Muscle;
MEDLINE=89210800; PubMed=3072195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 YIHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFEEEDF------QSMTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 RVLLTVLIAFTKKETSAV--AEAQKLMVQAADL-----LSAIHNSLHHGIQAQNDTTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 YLYNNHQAKDCIDSF-VTHCVRPF--CSLIQIHGHNRARQRDKLGHIL----EEFATLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  575 KKVRPLSREITMSQAYQNMCAGMFKTMVAFDMDGKVRKPKF------ELDSEQVRYEH
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                       273;
                                                                                                                                                                                                                                       Length 3660;
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                                                                        ZZ-TYPE.
MISSING.
Q -> H.
C -> H.
K -> M.
85493DAF6D5B6D4A CRC64;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QDFEEACRELKLGEL--LHDKLFGLFEAMSAIEMM-
                                                                                                                                                                                                                              3.1%; Score 117.5; DB 1;
17.7%; Pred. No. 6;
iive 113; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC1_HUMAN STANDARD; PRT; 736 AA. 014867; 042285; 15-JUL-1998 (Rel. 36, Created) 10-OKAY-2000 (Rel. 39, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
SPECTRIN 21.
SPECTRIN 22.
WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2208 RIESEKNILS-----EFQE--DLNK 2225
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                                                                                                                                                                                                                                                                                       Conservative 113;
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BAC1 HUMAN
ID BAC1 H
AC 014867
DT 15-JUL
DT 30-MAY
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MEDLINE=20289799; PubMed=10830953;

MEDLINE=20289799; PubMed=10830953;

Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,

Park H.-S., Toyoda A., Ishii K., Totokii Y., Choi D.-K., Garden Y.,

A Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,

B Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,

R Richwald K., Rump A., Schlilhabel M., Schudy A., Zimmermann W.,

R Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,

Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,

Minoshima S., Shimiqu N., Nordsiek G., Hornischer K., Brand P.,

Annoshima S., Shimiqu N., Rechelt J., Kauer G., Bloccker H.,

Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

Ramser J., Reinhardt R., Yaspo M.-L.;

RT The DNA sequence of human chromosome 21.";

Rature 405:311-319(2000).

C activator. Binds, in-vitro, to NF E2 binding sites Play important

C T. FUNCTION: Transcription activation and repression by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Taudien S., Dagand B., Delabar J., Nordsiek G., Drescher B., Weber J.,
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98140133; PubMed=9479503; Ohira M., Seki N., Nagase T., Ishikawa K., Nomura N., Ohara O.; Ohira M., Seki N., Nagase T., Ishikawa K., Nomura N., Ohara O.; "Characterization of a human homolog (BACHI) of the mouse Bachl gene encoding a BTB-basic leucine zipper transcription factor and its mapping to chromosome 21922.1."; Genomics 47:300-306(1998).
                                                                                                                                                                                     MEDLINE=98204399; PubMed=9544839;
Blouin J.-L., Duriaux Sail G., Guipponi M., Rossier C.,
Pappasavas M.-P., Antonarakis S.E.;
"Isolation of the human BACH1 transcription regulator gene, which
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Franscription regulator protein BACH1 (BTB and CNC homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the bZIP family. CNC subfamily.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taudien S., Dagand E., Delabar J., Nordsiek G., Drescher
Schattevoy R., Yaspo M.-L., Rosenthal A.,
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF026199; AAB84100.1; --
EMBL; AF026200; AAB84101.1; --
EMBL; AB002803; BAA24932.1; --
EMBL; AF124731; AAD14689.1; --
EMBL; AL163249; CAB90435.1; --
EMBL; AL0023; T00023.
FN92; P3477; 1SKN.
TRANSFAC; T04791; --
TRANSFAC; T04799; --
                                                                                                                                                                                                                                                                                maps to chromosome 21q22.1.";
Hum. Genet. 102:282-288(1998)
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MIM; 602751; -.
                                                             (Human)
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=9606;
                                                             Homo sapiens
                    (HA2303)
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316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 REDSSVASSDRSSVEREVAEHLAKGFWSDICSTDTPCQMQLSPAVAKDGSEQISQKRSEC 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 VELEHQQCLAVFSRVKFTRVLLTVLIAFTKK---ETSAVAEAQKLMVQAADLLSAIHNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSLSENSVFAYESSVHSTNVLLSLNDQRKKDVLCDVTIFVEGÖRFRAHRS-VLAACSSYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 HHGIQAQND----TTKGDHPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 HSRIVGQADGELNITLPEEVTVKGFEPLIQ-----FAYTAKLILSKENVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 --EVCKCVBFLSVBNIEESCFQFLKFKFLDSTADQQEC-----PRKKCFSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 L------MQDMVKDALRSFVD-PPVLSPKCYL---YNNHQAKDCIDSFVTHCVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 MC------LEKDAALALPSLCPKYRKFQKAFGTDRVRTGESSVKDIHASV--QPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 ERSENECLGGVPECRDLQVMLKCDESKLAMEPEETKKDPASQCPTEKSEVTPFPHNSSID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LYSMHEYYYIYWYLSEFLYAWLMSTLSRAD----GSQMAEERIMEEQQKG-RSSKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 IKTVÇEVVNLTNLHCILDFFCEF-----SEQSPÇVLSRSLLQTTFLVDNKKVFGTH
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.6%; Pred. No. 0.92;
ative 78; Mismatches 212; Indels 122;
                                                                                                           PEAM; PROGES; BTB; 1.
SMART; SMO0138; BTB; 1.
SMART; SMO0238; BTB; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS50197; BTB; 1.
PROSITE; PS00106; BZIP 1.
Transcription regulation; Activator; Repressor; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%; Score 116; DB 1; Length 736;
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30; GO:0003700; F:transcription factor activity; TAS.
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E -> G (IN REF. 1)
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30-MAY-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annocation update)
cleential phospholipid-transporting ATPase IH
class I type 11A) (ATPase IS)
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LEUCINE-ZIPPER.
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                           InterPro, IPR000210; BTB POZ.
InterPro, IPR008917; Buk_transcr_DNA
InterPro, IPR004827; TF_BZIP.
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607
158
171
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562
585
158
171
                                                                                                                                                                                                                                                                                                                                                       Nuclear protein.
DOMAIN 34
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P98197;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Found in heart, muscle, liver and brain.
Most abundant in heart. Also detected in fetal tissues.
SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
                                                                                                                                                       Halleck M.S., Lawler J.F. Jr., Blackshaw S., Gao L., Nagarajan P., Ardker C., Pyle S., Newman J.T., Nakanishi Y., Ando H., Weinstock P. Williamson P., Schlegel R.A., "Differential expression of putative transbilayer amphipath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Phosphorylation; Magnesium; ATP-binding;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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CYTOPLASMIC (POTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

135502 MW; 999A8BE19E9296C1 CRC64;
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                           transporters.";
Physiol. Genomics 1:139-150(1999).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
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PRINTS; PR00119; CATATPASE.
ITGREAMS; ITGR01652; ATPase-Plipid; 1.
TIGREAMS; ITGR01494; ATPASE PLYPE; 6.
PROSITE; PS00154; ATPASE E1 E2; 1.
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InterPro; IPR001757; ATBASE EL-B2.
InterPro; IPR00539; Flippase.
InterPro; IPR005834; Hydrolase.
                                                                                                                            MEDLINE=20473714; PubMed=11015572;
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                                                                           SEQUENCE FROM N.A.
STRAIN=ICR; TISSUE=Brain;
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Multigene family.
                        NCBI_TaxID=10090
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MEDLINE=97313266; PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Churcher C.M., Connor R., Devlin K., Gentles S., Hamin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
"The nuclectide sequence of Saccharomyces cerevisiae chromosome IX.";
Nature 387:84-87(1997).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 3.9;
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GO; GO:0005655; C:nuclear membrane; IDA.
GO; GO:0005654; C:nucleoplasm; IDA.
GO; GO:0006606; P:protein-nucleus import; IDA.
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Matches 142; Conservative 123;
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GermOnline; 139684; -.
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17;

Gaps

66; Mismatches 150; Indels 116;

3.0%; Score 115; DB 1; Length 1187; 0.2%; Pred. No. 2.1;

20.2%;

Similarity

Query Match Best Local (

Conservative

84;

Matches

ò g

92

34 QDFEEACRELKLGEL-LHDKLFGLFEAMSAIEMMDPKWDAGMIGNQVNRKVLNFEQAIKD

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9 DDDSGWELSMPEKMEKSNTNWVDITQDFEEACRELKLGEL--LHDKLFGLFEAMSAIEMM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 5.1;
86; Mismatches 215; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 113.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20223868; PubMed=10759889;
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Sporulation; Coiled coil.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 415:871-880(2002).
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Best Local Similarity
                                                             SEQUENCE FROM N.A.
 Ikemoto S., Naka
"S. pombe sporul
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                                      IEMMDPKMDAGMIGNQVNRKVL----NFEQAIKDGTIKIKDLTLPELIGIMDTCFCCLIT 118
                                                             ----ENKMDFSSKEGQYKAKIKELENNLERLRSDLQSKIQE-----IESIRSCKDSQLK 813
                                                                                                              ---NTIDDTEMKWKSL-----LTELSNKETTIEKLSSEIE 848
                                                                                                                                                             849 NLDKELRKTKFOYKFLDQNSDASTLEPTLRKELEQIQVQLKDANSQIQAYEEIISSNENA 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION. MEDLINE=20107136; Pubmed=10639340;
                                                                                      WLEGHSLAQTVFTCLYIHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFE
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
50cT-2003 (Rel. 42, Last annotation update)
Sportlation-specific protein 15.
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MEDLINE=21848401; PubMed=11859360;

We med V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

By Squros J., Peat N., Hayles J., Baker S., Basham D., Bowaman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin M., Davis P., Felewell T., Fraser A.,

Gontles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

Holroyd S., Hornsby T., Howarth S., Huchel E.J., Hunt S., Jagels K.,

Andres K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Holrory E., Mungall K., Murphy L., Niblett D., Odell C.,

RA Nitherford K., Rutter S., Sauders R., Sarey S.,

Rutherford K., Taylor K., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Taylor K., Taylor R., Tivey A., Walsh S.V., Warren T.,

RA Dordward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Lucas M., Rochet M., Gaillardin C., Palleda V.A., Garzon A., Thode G.,

Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Rominguez A., Revuelta J.L., Moreno S., Ammstrong J., Forsburg S.L.,

Rominguez A., Revuelta J.L., Moreno S., Ammstrong J., Forsburg S.L.,

Rominguez A., Revuel La J.L., Moreno S., Ammstrong J., Rorsburg S.L.,

Rominguez A., Revuel R., Sallardin C., Paulsen I., Potashkin J.,

Ry The genome sequence of Schizosaccharomyces pombe.";

Ry The genome sequence of Schizosaccharomyces pombe.";
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emoto S., Nakamura T., Kubo M., Shimoda C.;
. powhe spoulution-specific coiled-coil protein Spol5p is localized
the spindle pole body and essential for its modification.";
cell Sci. 113:545-554(200).
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-: FUNCTION: Has a role in the initiation of spore membrane
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-!- SUBCELLULAR LOCATION: Spindle pole body.
-!- SIMILARITY: Belongs to the MPC70 family.
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24;

Gaps

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1612 LAENERLSLTTRMLDLQNQVKD-----LSNIKDSLSEDLRTLRSLE----DSVASLQ-K 1660
                                                                                                                                                                            ---ELGRSKLKLASTTEELQ 1611
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                                                          DPK----MDAGMI----GNOVNRKVLNFEQAIKDGTIKIKDLT-----LPELIGIMDTCFC
                                                                                                                                      115 CLITWLEGHSLAQTVFTCLYIHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFEE--
                                                                                                                                                                                                                ----EDFQSMTYGFKMANSVTDLRVTGMLKDVEDDMORRVKSTRSRQGEERDPEVELEHQ
                                                                                                                                                                                                                                                                                          QCLAVFSRVKFTRVLLTVLIAFT----KKETSAVAEAQKLMVQAADLLSAIHNSLHHGIQA
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI TaxID=4932;
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Greenwell P.S., Kronmal S.L., Porter S.E., Gassenhuber J.,
Obermaler B., Petes T.D.,
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Putative phosphatidylinositol kinase involved controlling telomere length.
-!- SIMILARITY: Belongs to the Pl3/P14-kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obermaier B., Gassenhuber J., Piravandi E., Domdey H.; "Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevisiae chromosome II."; yeast 11:1103-1112(1995).
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01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
TELIOMER - Inegth requlation protein TELI.
TELI OR YELO88C OR YELO706.
Saccharomyces cerevisiae (Baker's yeast).
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01-07-2000 (TrEMBLrel. 15, Last sequence update)
01-07-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Corneal wound healing related protein.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
11,1
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MEDLINE=20314365; PubWed=10855038;
Yi X.J., Li X.F., Yu P.S.;
"A novel poithelial wound-related gene is abundantly expressed developing rat cornea and skin.";
Curr. Bye Res. 20:430-440(2000).
EMBL; AR272892, AAR81791.1; -.
Interpro; IPR007244; Mak10.
Pfam; PF04112; Mak10; 1.
SEQUENCE 725 AA; 83151 MW; ADB38695BDEICD2D CRC64;
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95.0%; Pred. No. 2.7e-297;
iive 15; Mismatches 14;
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Best Local
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SAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCLITWL 120
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                                     SAIEMMDPKMDAGMIGNQVNRKVLNFEQAVKDGTIKIKDLSLEPELIGIMDTCFCCLITWL
                                                                                                                                                                                                                                                                                     GFKWANGVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAAFSRVKFT
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                                                                                                                    EGHSLAQTVFTCLYIHNPDF1EDPAMKAFALG1LKICDIAREKVNKAAVFEEEDFQSMTY
                                                                                                                                                    GFKMANSVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFT
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae; Danio.
NCBI_TaxID=7955;
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Man S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
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                                                                                                                                                                                                                                                                                                                                                                                                         59
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernen R.J., McKernan K.J., Malek J.B., Mullahy S.J., Wilhards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y. Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                        DB 13; Length 724;
                                                                                                                                                                                                                                                                                                                     86.6%; Score 3331.5; DB 13; Lengt llarity 84.4%; Pred. No. 1e-270; Conservative 69; Mismatches 36; Indels
                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053286; AAH53286.1;
                                                                                                                                                                                                                                                                                              FBA6F44225F04B72 CRC64;
                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                            724 AA; 83152 MW;
                                                                                                                                                                    and mouse cDNA sequences."
                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                al Similarity
619; Conserv
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                            TISSUE=Kidney;
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652 ADLYMAASKHFQQAKLLLENVTSPDAEVNRILKVAKPNIVVMKLLAGGHKKETKALPEFD 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSPCVLSRSLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVSPPVLSPKCYLYNNHQAKDC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AEKVDAALH 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 EGHSLAQTVFTCLYIHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFEEEDFOSMTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGHSLAQTVFTCLYIHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFEEEDFQSMTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVMKASVDDDDSGWELSMPEKXMEKSNTNWVDITQDFEEACRELKLGELLHDKLFGLFEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCLITWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFKMANSVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFT
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Shibahara T.,
                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein FLJ21613.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawabatea A., Hikiji T., Kobatake N., Inagaki H., Ikema Y Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Sh Tanaka T., Nakamura Y., Isogai T., Sugano S., Tanaka T., Nakamura Y., Isogai T., Sugano S., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AK022266; BAB15097.1; -. InterPro; IPR072244; Mak10. Pfam; PF04112; Mak10; I. Hypothetical protein.

SEQUENCE 526 AA; 60382 MM; 084271691A886D50 CRC64;
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                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%; Score 2670; DB 4;
97.9%; Pred. No. 2.3e-215;
iive 1; Mismatches 2;
                                                                                                                                                                                                                                        PRT;
                                                                              Matches 514; Conservative
                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISSUE=Colon;
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Pred. No. 2.7e-102;

39.38;

Best Local Similarity

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KEXTANT=BERKEALEY;
RAM MEDILINE=20196006; PubMed=10731132;
RADATN=BERKEALEY;
RAM Amanatides FG., Scherer S.E., Holf R.A., Boskins R.A., Galle R.F.,
RAM Amanatides FG., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandlall M.D., Zhang O., Chen L.X.,
RAM Amanatides FG., Rogers Y.-H.C., Blazel, R.G., Champe M., Pfeiffer B.D.,
RAM ELLO G.G., Rogers Y.-H.C., Blazel, R.G., Champe M., Pfeiffer B.D.,
RAM Abril J.E., Robayani A., An H.-J., Andrews-Frankoch C., Bladwin D.,
RAM Abril J.E., Benos P.V., Bernard B.P., Bhandari D., Bolankavy S.,
Rameson K.Y., Benos P.V., Bernard B.P., Bhandari D., Bolankavy S.,
RAM Elevan M.R., Bouck J., Broketein P., Brothier P.,
RAM Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Center A., Chandra I.,
RAM Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Durbin K.J., Bavagelista C.C., Ferraz C., Ferraz C., Perriera S., Fleischmann W.,
RAM Glodek A., Gong F., Gornell J.H., Gu Z., Gulbart W.M., Glasser K.,
RAM Glodek A., Gong F., Gornell J.H., Gu Z., Gulbar P., Harris M.,
Allah M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McRherson D.L.,
RAM RAM Mount S.M., Murphy B., Murphy L., Murzny D.M., Nelson D.L.,
Ram B.E., Kodira C.D., Kraft C., Kratt E., Mortis J., Nosher S.,
Rount S.M., Moy M. Wurphy B., Murphy L., Murzny D.M., Nelson D.L.,
Ram Spier E., Spradling A.C., Pan S., Pollard J., Weissenbach J.,
Rhenert K., Remington K., Saunders R., On Weissenbach J.,
Syrickas R., Mosamm D.A., Weinsched S., Zhu X., Smith H.O.,
Rheng R., Zhong R., Zhong W., Zhong K., Zhu X., Smith H.O.,
Rheng R., Zhong R., Rubin G.M., Wang S., Yao Q.A.,
Rheng R., Zhong R., Rubin G.M., Wang S., Zhu X., Smith H.S.,
Rheng R., Zhong R., Rubin G.M., Wang S., Zhu X., Smith H.S.,
Rheng R., Zhong R., Rubin G.M., Wang S., Zhu X., Smith H.S.,
Rheng R., Zhong R., Rubin G.M., Wang S., Ch., Shon R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stapleton M.A. Brokstein P., Hong L., Agbayani A., Carlson J., Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liso G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., houanenavong S., Wan K., Submitted (CGT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AZ003463; AARF47171.1; -
EMBL, AZ003463; AAL204961; -
FlyBase; FBgn0034982; CG4065.
InterPro; IPR007244; Max10.
                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota,
Neoptera; Endopteraygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DBDB966F0F523F17 CRC64;
                                                                                                                                                                         (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                       784 AA
                                                                                                                                               Created)
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                                                                   PRELIMINARY;
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NCBI_TaxID=7227;
                                                                                                                                           01-MAY-2000
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01-JUN-2003
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RESULT
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Length 784;

DB 5;

Score 1326;

34.5%;

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14;
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                                                                                              89 AIXDGTIKIKDLTLPELIGIMDTCFCCLITWLEGHSLAQTVFTCLYIHNPDFIEDPAMKA 148
                                                                                                                                                                                                                                                                                                             KREEMVNYFARLIDRIKTVCEVVNLTNLHCILDFFCEFSEQS-PCVLSRSLLQTTFLVDN 379
                                                                                                                                                                                                                                                                                                                                                                        361 DRPSSYQFLEEMISRFKYACKVTKYKDYYSALNFFIEYSKKSGQCILSRSVLQTLFSANM 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POR---QHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFLYAWLMST 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSRADGSQMAEERIMEEQQKGRS-----SKKTKKKKKKRPLSREITMSQAYQNM 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTRTENILLÁQEEYAEHÓSKTQSGGGAAKNRKAAKPKKNKKTQRÞYRAEIVFYHÁLLSL 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYSPPPQSPELYVAASKHFQQAKMILENIPNPDHEVNRILKVAKPNFVVMKLLAGGHKKE 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::| ::|| |:|| ||:|| ||: ||:|| ||: ||:|| ||: ||-||:|| ||:|| ||:|| ||:|| ||:|| RHS----VEDLYTYAARKHFDQARNVLESIONPDQEMLDLLQIARTNFVVMNVLARGHQKE 763
                               88
                                                  80 WYDVTKEFHDACAELQPGELAQDMLFGLFEAMSAIEIMDFKMDVGMGFDKQDLPPPSFEA
                                                                                                                200 FCTAVRNLIVVIKKIIAVAAVNEEEDFQ--LYGNSALLAAEKAQPATVYSSLKDVEDELI
                                                                                                                                                                                                                                                258 RKCKKLTST-------BDWAVVHRLRFWRHLFQVIYHVEQMASNDTVDDKVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                           29 WVDITQDFEEACRELKLGELLHDKLFGLFEAMSAIEMMDPKMDAGMIGNQVNRKVLNFEQ
                                                                                                                                                          149 FALGILKICDIAREKVNKAAVFEEEDFQSMTYG---FKMANSVTDLRVTGMLKDVEDDMQ
                                                                                                                                                                                                                          206 RRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQ---
                                                                                                                                                                                                                                                                                          263 -KLMVQAADLLSAIHNSLHHGIQAQNDTTKG-DHPIMMGFEPLVNQKLLPPFFPRYAKII
                                                                                                                                                                                                                                                                                                                                                                                                                       KKVFGTHLMQDMVKDALRSFVDPPVLSPKCYLYNNHQAKDCIDSFVTHCV--RPFCSLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGMEKTMVAFDMDGKVRKPKFELDSEQVRYEHRFAPFNSVMTPPPVHYLQFKEMSD-LN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tashiro H., Ota T.,
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-007-2002 (TERMELTEL 22, Last annotation update)
Hypothetical protein FLJ22643.
Hypothetical protein FLJ22643.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDAALHTMLLKQ-----
 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Small intestine;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro I
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Mismatches 246; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKVPPEFDFSAHKYFPVVKL 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKRQPEFDFSKHSYFPIIKL 783
 291; Conservative 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9H631;
01-MAR-2001
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   Matches
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RRVKSTRSRQGEERDPEVELEHOOCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQ--- 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SKKTKKKKKVRPLSREITMSQAYQNM 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587 LTRTENILLAQEEYAEHQSKTQSGGSGAAKNRKAAKPKKNKKTQRPYRAEIVFYHALLSL 646
                                                                                                                                                                    KREEMVNYFARLIDRIKTVCEVVNLTNLHCILDFFCEFSEQS-PCVLSRSLLQTTFLVDN 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ITMSQAYQNMCAGMFKTWVAFDMDGKVRKPKFGLDSEQVRYEHRFAPFNSVMTPPPVHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            644 QFKEMSDLNKYSPPPQSPELYVAASKHFQQAKMILENIPNPDHEVNRILKVAKPNFVVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           584 ITMSQAYQNMCAGMFKTMVAFDMDGKVRKPKFELDSEQVRYEHRFAPFNSVMTPPPVHYL
                            ---EDWMAVVHRLRFMRHLFQVIYHVEQMASNDTVDDKVDI
                                                                                                         PQR----QHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFLYAWLMST
                                                                                 -KLMVQAADLLSAIHNSLHHGIQAQNDTTKG-DHPIMMGFEPLVNQRLLPPTFPRYAKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
BMBL; AK039316; BAC30316.1; -.
MGD; MGI:2441791; A330021G12Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                      438 IHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDAALHTMLLKQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Corneal wound HEALING related protein homolog (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 150 AA; 17236 MW; 703BD7A706353982 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.1%; Score 772; DB 11; 97.3%; Pred. No. 8.8e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  704 LLAGGHKKESKVPPEFDFSAHKYFPVVKLV 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Spinal cord;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSRADGSQMAEERIMEEQQKGRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647 CGGMYKAMGALTKDGRVR 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                           257 RKCKKLTST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBBYJ9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FCTAVRNLIVVIKKIIAVAAVNEEEDFQ--LYGNSALLAAEKAQPATVYSSLKDVEDELI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 AIKDGTIKIKDLTLPELIGIMDTCFCCLITWLEGHSLAQTVFTCLYIHNPDFIEDPAMKA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FALGILKICDIAREKVNKAAVFEEEDFQSMTYG---FKMANSVTDLRVTGMLKDVEDDMQ 205
                                                                                                                                                                                                                                                                                                                                                            EITMSQAYQNMCAGMFKTMVAFDMDGKVRKPKFELDSEQVRYEHRFAPFNSVMTPPPVHY 120
                                                                                                                                                                                                                                                                                                                                                                                                        LOFKEMSDLNKYSPPPQSPELYVAASKHFQQAKMILENIPNPDHEVNRILKVAKPNFVVM 702
                                                                                                                                                                                                                                                                                                                                                                                                                                LQFKEMSDLNKYSPPPQSPELYVAASKHFQQAKMILENIPNPDHEVNRILKVAKPNFVVM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 AIATGAIKLDDLTPSELIGIXDALFSCLVSWLEGNSMDQVLFTCLYLHAPAQIKDKALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 WVDITQDFEEACRELKLGELLHDKLFGLFEAMSAIEMMDPKMDAGMIGNQVNRKVLNFEQ
                                                                                                                                                                                                                                                                             1 MHEYYYIYWYLSEFLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSR
                                                                                                                                                                                                                                     523 MHEYYYIYWYLSEFLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKVRPLSR
                                                                                                                                                                                                                                                                                                                       EITMSQAYQNMCAGMFKTMVAFDMDGKVRKPKFELDSEQVRYEHRFAPFNSVMTPPPVHY
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukoryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                            / Match 29.0%; Score 1116; DB 4; Length 211; Local Similarity 100.0%; Pred. No. 1.9e-85; les 211; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity 37.7%; Pred. No. 1.9e-76; 233; Conservative 104; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celniker S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
  Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (400-2000) to the EMBL/GenBank/DDBU databases EMBL, AK026296; BAB15435.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF04112; Mak10; 1.
SEQUENCE 708 AA; 79791 MW; 181B7154C9C0C137 CRC64;
                                                                                   Hypothetical protein.
SEOUENCE 211 AA; 24786 MW; FGESBEFB66A6B77E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLLAGGHKKESKVPPEFDFSAHKYFPVVKLV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLLAGGHKKESKVPPEFDFSAHKYFPVVKLV 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           708 AA
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InterPro; IPR007244; Mak10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8T3X5;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
AT26759p.
CG4065.
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MEDLINE-99069613; PubMed-9851916;
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Science 282:2012-2018(1998),
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Hypothetical protein.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; rosids;
eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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PIR; B84495; B84495.
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SEQUENCE 695 AA; 78885 M
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Davidson S., Wohldmann P., Gillam B.;
"The sequence of C. elegans cosmid T23B12.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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"Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; #R202981; AAB69936.2; -.
PIR; T32223, T32223.
WormPep; T23B12.4; CE29351.
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Last sequence update)
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                                                                                                                                                       QVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCLITWLEGHSLAQTVFTCLYIHN 137
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                                                              18 MPEKWEKSNTNWVDITQDFEEACRELKLGELLHDKLFGLFEAMSAIEMMDPKMDAGMIGN
                                                                                          Gaps
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                       Matches 204; Conservative 134; Mismatches 302; Indels 179;
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                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                   German Neurospora genome project;
Submirted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL669968; CAD21048.1;
InterPro; IPR007244; Mak10.
IPfam; PF04112; Mak10;
Hypochetical protein.
SEQUENCE 908 AA; 101120 MW; D40AF51D21542FF6 CRC64;
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                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 21.5%; Pred. No. 1.4e-22;
Matches 162; Conservative 106; Mismatches 277;
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21.5%; Pred. No. 1.4e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oliver K., Harris D., Lyne M.H., Rajandream M.A., Barrell B.G., Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL109834; CAB52739.1; -. PIR; T39742; T39742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 175;
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                                                                                                                                                                                     Hypothetical protein. Spring amount on update; SPBC1861.03. Schizosaccharomyces pombe (Fission yeast). Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaces;
                                                                                                                                                        Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.6%; Score 252.5; DB 3; Best Local Similarity 18.7%; Pred. No. 3.1e-12; Matches 143; Conservative 143; Mismatches 302;
                                                                                                                          sequence update)
    708 AA
                                                                                Created)
    PRT;
                                                                                                                          Last
                                                                       (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 25, L
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InterPro; IPR007244; Mak10.
Pfam; PF04112; Mak10; 1.
Hypothetical protein.
PRELIMINARY;
                                                                   01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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708 AA; 8
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NCBI_TaxID=4896;
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                                                       MEDLINE-22255708; PubMed=1236867;

MEDLINE-22255708; PubMed=1236867;

Hall N., Pain A., Beriman M., Churcher C., Harris B., Harris D.,

Hall N., Pain A., Beriman M., Churcher S., Barron A., Brooks K.,

Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,

A chilingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,

Croil A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,

Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Harper D., Hauser H., Horrsby T., Holroyd S., Horrocks P.,

Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

Line A., Maddison M., Molean J., Mooney P., Mulby L.,

And Andison M., Mclean J., Mooney P., Mulby L.,

And Andison M., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,

Seeger K., Sharp S., Smith R., Squares S., Stevens K.,

Rajandream M.A., Rutter S., Rutherford S., Woodward J.,

Sulston J.E., Craig A., Nowbold C., Barrell B.G.,

"Laylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,

"Laylor Craig A., Newbold C., Barrell B.G.,

"Laylor R., Paris M., Rutter S., Rutherford S., Woodward J.,

"Laylor R., Fivey A., Unwin L., Whitehead S., Woodward J.,

"Laylor R., Paris M., Rutter S., Rutherford S., Woodward J.,

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CS7BL/6;
Wenzlau J.M., Weiser-Evans M.C.M.;
Wouse Embryonic Growth Associated Protein Promotor Sequence.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=36329;
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Embryonic growth-associated protein EGAP (Fragment)
Bukarvet. V.
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Pred. No. 1.1e-08;
5; Mismatches 2;
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                                                                                                                                            ---NPDFIEDPA 145
                                                                                                                                                            MK---AFALGILKICDIAREKVNKAAV--FEEDFOSMTYGFKMANSVTDLRVTGMLKDV 200
                                                                                                                                                                                                                    MKWLAAFSYDKIYM-DIFKND-NKEFIKYIEKHDDQKKNFN---KNKVADNK-----KDS 179
                                                                                                                                                                                                                                            BDD--MQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAV 258
                                                                                                                                                                                                                                                                 -----KKSDTI 207
                                                                                                                                                                                                                                                                                           259 AEAQKLMVQAADILSAIHNSIHHGIQAQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRYAK 318
                                                                                                                                                                                                                                                                                                                                          319 II--KREEMVNYFA---RLIDRIKTVCEVVNLT----------NL----HCILD 353
                                                                                                                                                                                                                                                                                                                                                                 JFYSSSSELIDYVITONNFVHRDDYKCGLVNLADCLLYHCRNRRAYILKNLFIIKRCFTK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                          399 FVDPPVLSPKCYLYNNHQAKDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFA 458
                                                                                                                   74
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                                                                                                                                                                                                                                                                                                                                                                                            -- VFGTHLMQDMVKDALRS
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                                                                                                           TLODE---FMTFYFNRAEKVDAALHTMLLKQEPQRQHLACLGT---WULYHNLRIMIQYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----nvesgknnscpilankfntknekredlesdk
                                                                                            42 ELKLGELLHDKLFGLFEAMSAIEMMDPKMDAGM-----IGNQVNRKVLNFEQAIKDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ol-OCI-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DKEZP434B168-like protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygai; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBL TaxID=7955;
                                                                   224;
                                                                     216; Indels
            Hypothetical protein.
SEQUENCE 1218 AA; 147226 MW; 7A081A9B4D0E10ED CRC64;
                                                                                                                                            IKIKDLTLPELIGIMDICFCCLITWLEGHSLAQTVFTCLYIH----
                                            Query Match 3.9%; Score 150; DB 5; Best Local Similarity 19.4%; Pred. No. 0.0027; Matches 131; Conservative 106; Mismatches 216
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EMBL; AL929356; CAD51797.1;
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                 E., Chen W.,
Nissen R.M.,
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                                                                                                                                                                                                                                                                                                                                                  Indels 355;
                                                                                                "Insertional mutagenesis in zebrafish rapidly identifies genes essential for early vertebrate development.";
Nat. Genet. 31:135-140(2002).
EMBL; AYO9529; AAW2517.1; -.
InterPro; IPR008938; ARM.
SEQUENCE 964 AA; 106914 MW; 280310F72EADDAAA CRC64;
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Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y.,
Hopkins N.;
                                                                                                                                                                                                                                                                                            Length
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Matches 182; Conserv
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8 G

Search completed: August 10, 2004, 21:51:28 Job time : 47 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

ws gnisu - protein search, OM protein

August 10, 2004, 21:44:16; Search time 58 Seconds (without alignments) 3570.816 Million cell updates/sec Run on:

US-10-001-857-145 3849 1 MVWKASVDDDDSGWELSMPE......KVPPEFDFSAHKYFPVVKLV 733 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
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geneseqp2003as:* Geneseq 29Jan04:* geneseqp2004s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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115	115	115	115	114.5	114.5	114.5	114.5	114.5	114.5	114	114	114	114	114	114	114	114
26	28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Human lung specific protein sequence SEQ ID NO:145. ABP52902 standard; protein; 733 AA. (first entry) 05-NOV-2002 ABP52902; RESULT 1 

Human; lung; lung specific nucleic acid; LSNA; lung specific protein; LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer; squamous cell carcinoma.

Homo

WO200264788-A2.

22-AUG-2002.

20-NOV-2001; 2001WO-US045080.

(DIAD-) DIADEXUS INC

20-NOV-2000; 2000US-0252054P.

ΰ Liu Sun Y, Chen S, Recipon H, Macina RA,

WPI; 2002-657601/70.

New lung specific nucleic acid useful in gene therapy or as vaccines for treating lung cancer (e.g. squamous cell carcinoma) or non-cancerous lung diseases, as well as for diagnosing, monitoring or staging these diseases.

Claim 11; Page 239-242; 282pp; English.

The present invention describes an isolated lung specific nucleic acid (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid sequences comprising 17 - 733 amino acids, given in ABPES873 to ABPES965; (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b); or (d) has 60 % sequence identity to (a) or (b). LSNA and LSPS sequences have cytostatic activity and can be used in gene protein (LSP) sequences have cytostatic activity and can be used in gene monitoring the presence and metastases of lung cancer in a patient. An antibody that specifically binds to an LSP can be used for determining the presence of an LSP in a sample, as well as for treating a patient

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molecule for disease detection and treatment protein
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with lung cancer, particularly by inducing an immune response against the lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs and LSPs are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-cancerous disease states in lung
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                                                                                                                                  Query Match
Best Local Similarity
These 733; Conserve
                                                                                                                    Sequence 733 AA;
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The present invention relates to human proteins and coding sequences of molecules for disease detection and treatment MDDT. The sequences can be used in the treatment of diseases associated with the decreased expression or overexpression of MDDT, such as cell proliferative (cancer, atherosclerosis, hepatitis), autoimmune/inflammatory (e.g. AIDS, allergies, Addison's disease, asthma), developmental (dwarfism, renal tubular acidosis), neurological (e.g. stroke, Parkinson's disease, epilepsy) and cardiovascular (congestive heart failure, myocardial infertion, angina pectoris) disorders. The present sequence is a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human molecules for disease detection and treatment (MDDT), useful diagnosing, treating and preventing diseases or conditions associated the aberrant MDDT expression, e.g. cancer, AIDS, asthma, diabetes,
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Human; molecule for disease detection and treatment; MDDT; gene therapy cytostatic; antiarteriosclerotic; hepatotropic; anti-HIV; antiallergic; antiinflammatory; antiasthmatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; cardiant; antianginal.
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Ding L, Gietzen KJ, Ison CH, Lu DAM;
AR, Thangavelu K, Sanjanwala MM, Tang YT
JA, Swarnaker A, Azimzai Y, Sapperstein S
Lu Y, Tran UK, Marquis JP;
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Pred. No. 0;
0; Mismatches
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2001US-0271118P.
2001US-0274486P.
2001US-0374436P.
2001US-0334239P.
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Best Local Similarity 98.8
Matches 724; Conservative
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Ghandi A
Griffin d
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Honchell CD, Yue H
Hafalia AJA, Ghand
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09-MAR-2001;
28-NOV-2001;
01-FEB-2002;
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23-FEB-2001;
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                         RVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGF 300
                                                                                                                      QSPCVLSRSLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVDPPVLSPKCYLYNNHQAKDC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemla; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic;
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RVLLTVLIAFTKKETSAVABAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang Z,
                                                                                                                                                                                                       Human novel polypeptide sequence, SEQ ID NO:1094.
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Zhou P, Ghosh M, Wang D, Ma Y, Asundi V,
Haley-Vicente D, Drmanac RT;
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The invention relates to 971 novel human CDMA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The ADC30889 and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDMAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody compained by the invention; and methods of polymucleotides or polypeptides of the invention; and methods of invention are methods of peventing, treating or ameliorating a medical condition; kits comprising polymucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polymucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDMA sequences of the invention or activity of the polymucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDMA sequences of the invention or activity of the polymptides encoded by the contigs (ADC32628 - ADC33394). The nucleic acids and polypeptides encoded by the contigs (ADC32628 - ADC33394). The nucleic acids and polypeptides of the invention are context of identification of mutations responsible for genetic disorders or other traits, for assessing blodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disparses and other neurodegenerative diseases, andemed or treating diseases such as Parkinson's disease, Alzheimer's disparse or accorded by the control or accorded by the control or accorded by the control or accorded by the control or accorded by the control or accorded by the control or accorded by the control or accorded by the control or accorded by the control or accorded by the control or accor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence was obtained in electronic formmat directly from WIPO at the wipo.int/pub/published_pct_sequences.
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nes 718; Conservative
WPI; 2003-371981/35.
N-PSDB; ADC30041.
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ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                       WLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREITMSQAYQNMCAGMFK
             HTMLLKQEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFLYA
                                                                                                          HTMLLKQEPQRQHLAWLGTWVLYHNLRIMIQYLLSGFELYSMHEYYYIYWYLSEFLYA
                                                                                                                                   WLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREITMSQAYQNMCAGMFK
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QSPCVLSRSLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVD-PPVLSPKCYLYNNHQAKD
                                          CIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEBFATLQDBFMTFYFNRAEKVDAAL
                                                                                                                                                                               TMVAFDMDGKVRKPKFELDSEQVRYEHRFAPFNSVMTPPPVHYLQFKEMSDLNKYSPPPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 7956; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 7956
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2000US-00614150.
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                                                      Indels
                         Query Match 34.5%; Score 1326; DB 4; Best Local Similarity 39.3%; Pred. No. 2.4e-122; Matches 291; Conservative 131; Mismatches 246;
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cell

bursitis, cirrhosis, hepatitis, polycythaemia vera, anaemia, psoriasis; bursitis, cirrhosis, hepatitis, polycythaemia vera, anaemia, psoriasis; porimary thrombocytopenia, cancer, adenocarcinoma, leukaemia, myeloma, sarcoma, immune system disorder, acquired immunodeficiency syndrome, AIDS, allergy, asthma, Crohn's disease, diabetes mellitus; gout; glomerullonephritis, Goodpasture's syndrome; thyroiditis, pancreatitis, hepatitis, multiple solerosis, osteoporosis, Reiter's syndrome; rheumatoid arthritis, neurological disorder; epilepsy, stroke, dementia, Albahamer's disease; pick's disease; huntington's disease; mond; anxiety, Parkinson's disease; central nervous system disorder; mental disorder; schizophrenic disorder; amnesia, Tourette's disorder; transgenic animal; secretory polypeptide; SPTM; actinic keratosis; arteriosclerosis; WPI; 2002-590716/63. WO200257304-A2. gene therapy. Homo sapiens. 25-JUL-2002 

, 2001US-0261864P. , 2001US-0261865P. , 2001US-026191P. , 2001US-0262164P. , 2001US-0262164P. , 2001US-026218P. , 2001US-026208P. , 2001US-026259P. , 2001US-026229P. 2001US-0263063P. 2001US-0263066P. 2001US-0263069P. 19-JAN-2001; 2001US-0263074P. 19-JAN-2001; 2001US-0263076P. 19-JAN-2001; 2001US-0263077P. 15-JAN-2002; 2002WO-US001340. 2001US-0263070P. 19-JAN-2001; 2001US-0263329P 19-JAN-2001; 19-JAN-2001; 17-JAN-2001; 19-JAN-2001; 19-JAN-2001; 19-JAN-2001; 17-JAN-2001; 17-JAN-2001; 19-JAN-2001; 16-JAN-2001; 16-JAN-2001; 16-JAN-2001; 16-JAN-2001;

(INCY-) INCYTE GENOMICS INC.

Jones AL; Chen AJ; Dufour GE, Hillman JL, V, Daffo A, Marwaha R, David MH, Lewis SA; Dam TC, Liu TF, Harris B, Flores Chang SC, Gerstin EH, Peralta CH, Lincoln SE, Altus CM, Panzer SR,

N-PSDB; ABS51309

New purified secretory polypeptides and polynucleotides, useful in the diagnosis, study, prevention or treatment of diseases associated with decreased expression of functional secretory molecules, e.g. AIDS, cancer or allergies

Claim 27; Page 304-305; 340pp; English.

The invention describes an isolated polynucleotide a naturally occurring polynucleotide sequence at least 90 % identical to it, a polynucleotide complementary to it or an RNA equivalent of it. The purified secretory polypeptides (SPTW) and polynucleotides are useful in the diagnosis, study, prevention or treatment of diseases associated with decreased expression of functional SPTW, e.g. actinic Keratosis, arteriosclerosis, bursitis, oirrhosis, hepatitis, olycythemia vera, primary thrombocytopenia, anaemia, psoriasis, cancers including adenocarcinoma, thrombocytopenia, anaemia, psoriasis, cancers including adenocarcinoma, leukaemia, myeloma or sarcoma, immune system disorder such as acquired immunodeficiency syndrome (AIDS), allergies, asthma, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Hashimoto's thyroiditis, hepatitis, multiple sclerosis, osteoporosis, pancreatitis, Reiter's syndrome, autoimmune thyroiditis or rheumatoid arthritis, neurological disorders such as epilepsy, stroke, Alzheimer's disease, other developmental disorder of the central nervous system, mental disorder including mood, anxiety or schizophrenic disorder, mental disorder. The polynucleotides may be used in

Example 2; SEQ ID NO 2818; 1185pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147
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hybridisation and amplification technologies, e.g. in assessing gene expression patterns, to develop a transcript image for a particular cell or tissue, or to create transgenic animals to model human disease. This is the amino acid sequence of a human secretory protein isolated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCLITWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WWKASVDDDDSGWELSMPEKMEKSNTNWVDITQDFEEACRELKLGELLHDKLFGLFEAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human novel contig-encoded polypeptide sequence, SEQ ID NO:2818.
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                                                                                                                                                                                                                                                                             Length 239;
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                                                                                                                                                                                                                                                                         28.6%; Score 1100; DB 5; 99.5%; Pred. No. 1.2e-100;
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Asundi V,
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Zhou P, Ghosh M, Wang D, Ma Y, A
Haley-Vicente D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC32736 standard; protein; 160 AA
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                                                                                                                                                                                                                                                                                                                                            Matches 211; Conservative
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                                                                                                                                                                                                             Sequence 239 AA;
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99GB-00000167.

06-JAN-1999;

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Markham AF, Bonthron 2000-465983/40.

N-PSDB; AAA58824

(UYLE-) UNIV LEEDS.

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The invention the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the nuclein and compasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody capability and compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or invention further discloses methods of peventing, treating or ameliocating a medical condition, kits comprising polymoclectide probes and/or monoclonal antibodies for carrying out the methods of the invention of antibodies for carrying out the methods of the invention are and/or monoclonal antibodies for carrying out the methods of the invention or activity of the polymolectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are appropriated and polypeptides encoded by the contigs (ADC32628 ADC33841. The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, foresists, genemic disorders or other capacits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and maino acid sequences. They are also used for treating diseases und amino acid sequences or cancer The mucleic acids and produces, pathoparcs, antenna, placelet the mucleic acids and animo acid sequences or their capaciders, woundes, burns, ulcers, osteoporosis, autominance or and scales or and disorders, which is a supported and an acids and animo acid sequences or and sorders or other and should be acids and other neurodegenerative diseases, anaemia, placelet and other neurodegenerative diseases, anaemia, placelet and animo acids and animo acids and animo acids and animo acids and animo acids and acids and animo acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and as food supplements. The present sequence represents a human contigencoded polypeptide sequence used in an example of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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100.0%; Pred. No. ...
0; Mismatches
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The present sequence represents a murine tissue repair protein. Tissue repair gene polymucleotides are useful for determining expression of mRNA in selected target tissue, e.g. for diagnosing and treating orofacial clefting. They are also useful for determining the presence of DNA mutations in parients suffering from, or suspected to be suffering from orofacial clefting. The antibodies are also useful in the diagnosis of orofacial clefting. The polymucleotide is also useful for promoting wound

healing and tissue repair

New human and mouse nucleic acids encoding a tissue repair protein, useful for diagnosing and treating orofacial clefting, and for promoting wound healing and/or tissue repair.

Claim 22; Fig 8; 45pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VQAADLLSAIHNSLHHGIQAQNDTTKGDHP-----IMMGFEPL--- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 LPLSYVTDAPDATVADMLQDVYHVVTLKİQLQSCSKLEDLPABQWNHATVRNALKELLKE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNQSTLAKECPLSQSMISSIVNSTYYANVSATKCQEFGRWYKKYKKIKVERVERENLSDY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CILDFFCEFSEQSPCVLSR----SLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVDPPV 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDAALHTMLLKQEPQRQHLAC 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVVQLPPEPVQVLHRQQSQPTKESSPPREBAPPPPPTEDSCAKKPRSRTKISLEALGIL 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- RLIDRIKTV-CEVVNLTNL--H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 VEVSPDIYQQVRDE----LKRASVSQAVFARVAFNRTQ---GLLSEILRKEEDPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 NSVMTPP-PVHYLQ-----FKEMSDLNKYSPPPQSPELYVAASKHFQQAKMILENIP--
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                          Score 127; DB 3; Length 733;
Pred. No. 0.0076;
L; Mismatches 227; Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                217 BERDPEVEL----EHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 LGTWVLYHNLRIMIQYLLSGFELE---LY-----SMHEYYYIYWYLSE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNQRLLPPTFPRYAKI IKREEMVNYFA-
                                                                                                                                                                                                                                                                                                                                                                                      91;
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                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 20.9*
Matches 132; Conservative
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Tissue repair protein; orofacial clefting; wound healing; tissue repair.

06-JAN-2000; 2000WO-GB000003

WO200040719-A2.

Mus sp

13-JUL-2000

Amino acid sequence of a murine tissue repair protein.

405

464 574 682

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The invention relates to compositions and methods for the diagnosis and therapy of cancer, particularly colon cancer. The invention also provides colon tumour proteins and to polymucleotides encoding such proteins. Polymucleotides of the invention are useful for preventing, diagnosing and/or treating cancer, particularly colon cancer in a patient. They are used in gene therapy and also to prepare vaccines. The present sequence is human colon tumour protein
                                                                                                                                                                                                                                                                                                                                                                           570 HVVQLPPEPVQVLHRQQSQPAKESSPPREEAPPPPPPPPPDSCAKKPRSRTKISLEALGIL 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide useful for stimulating and/or expanding T-cells specific for a tumor protein, and preventing, diagnosing and/or
                                                                                                465 TSTPTTDLPIKVDGANINITAAIYDEIQQEMKRAKVSQALFAKVAANKSQGWLCELLRWK
                                                                                                                                                                                                                                             KKVRPLSREITMSQAYQNMCAGMFKTMVAFDMDGKVRKPKFELD---SEQVRYBHRFAPF
                                                                                                                                                                                                                                                                        632 NSVMTPP-PVHYLQ-----FKEMSDLNKYSPPPQSPELYVAASKHFQQAKMILENIP--
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Best Local Similarity 20.9%; Pred. No. 0.008;
Matches 132; Conservative 91; Mismatches 227; Indels 182; Gaps
358 VEVSPDIYQQVRDE----LKRASVSQAVFARVAFNRTQ----GLLSEILRKEEDPR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon tumour protein; cancer; gene therapy; vaccine.
                                                                  SMHEYYYIYWYLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells specific for a tumor protein, and preventing, diag
treating cancer, particularly colon cancer, in patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour protein from clone, C1562P KIAA1034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSFIHDVGLYPDQEAIHTLSAQLDLPKHTIIK 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 146-148; 158pp; English.
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                                                                  496 LGTWVLYHNLRIMIQYLLSGFELE-
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21-DEC-2001; 2001US-0343517P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE36464 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 LPLSYVTDAPDATVADMLQDVYHVVTLKIQLQSCSKLEDLPAEQWNHATVRNALKELLKE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------RLIDRIKTV-CEVVNLTNL--H 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 IQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDAALHTMLLKQEPQRQHLAC 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human and mouse nucleic acids encoding a tissue repair protein, useful for diagnosing and treating orofacial clefting, and for promoting wound healing and/or tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repair gene polynucleotides are useful for determining expression of mRN in selected target tissue, e.g. for diagnosing and treating coofacial clefting. They are also useful for determining the presence of DNA mutations in patients suffering from, or suspected to be suffering from corforaial clefting. The antibodies are also useful in the diagnosis of orofacial clefting. The polynucleotide is also useful for promoting woun healing and tissue repair
                                                                                                                                                                                                                                                                    Tissue repair protein; orofacial clefting; wound healing; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 MNOSTLAKECPLSOSMISSIVNSTYYANVSATKCOEFGRWYKKYKKIKVERVERENLSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --HQAKDCID-SFVTH-----CVR--PFCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a human tissue repair protein. Tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3%; Score 127; DB 3; Length 733; 20.9%; Pred. No. 0.0076; ive 91; Mismatches 227; Indels 182;
                                                                                                                                                                                                                          Amino acid sequence of a human tissue repair protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNQRLLPPTFPRYAKIIKREEMVNYFA-
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                                                                                            standard; protein; 733 AA
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Best Local Similarity 20.9°
Matches 132, Conservative
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N-PSDB; AAA58823.
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                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CYLYNN-----HQAKDCID-SFVTH-----CVR--PFCSL
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                                                                                                                                                                                                                                                --RLIDRIKTV-CEVVNLTNL--H
                                                                                                                                                                                                                                                                                                  214 MNOSTLAKECPLSQSMISSIVNSTYYANVSATKCQEFGRWYKKYKKIKVERVERENLSDY
                                                                                                                                                                                                                                                                                                                                                                 CILDFFCEFSEQSPCVLSR----SLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVDPPV
                                                                                                                                                                                                                                                                                                                                                                                                                       CVLG------QRPMHLPNMNQLASLGKTNEQSPHSQIHHSTPIRNQV-PALQPIMSPGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKVRPLSREITMSQAYQNMCAGMFKTMVAFDMDGKVRKPKFELD---SEQVRYEHRFAPF
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protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                           ---IMMGFEPL-
   ---EHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGTWVLYHNLRIMIQYLLSGFELE---LY-----SMHEYYYIYWYLSE-----
                                                                                                                        --VQAADLLSAIHNSLHHGIQAQNDTTKGDHP-
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The present invention describes a predictor set comprising a plurality of polymucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. Also described: (1) predicting whether a compound is capable of medulating the activity of cells, comprising obtaining a sample of cells, determining whether the cells express a plurality of markers, and correlating the expression of the markers to the compound's ability to correlating the expression of the markers to the compound's ability to correlate the activity of the cells; (2) a plurality of cell lines for identifying polymucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state, and (3) identifying polymucleotides and collypeptides that predict compound sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of cells interest of coll interest of compounds, analysing the expression pattern of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a microarray of polynucleotides or polypeptides, and selecting polynucleotides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides any polynucleotides have cytostatic activities, and can be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: | : | : | | : | | : : EQLDGSLEYDNREHAEFVLVRKDVLFSQLVETALLALGYSHSSA-AQAQGIIKLGRWNP
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                                                                                       polynucleotides and polypeptides for predicting the activity of bounds that interact with protein tyrosine kinases and/or protein
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!; Mismatches 227; Indels 182;
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                                                                                                                                                                               Claim 10; SEQ ID NO 380; 139pp; English.
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257 AVAEAQKIMVQAADILSAIHNSIHHGIQAQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRY 316
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                                                       --RVTGM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDA 477
137 ITRVKGN---LRVFTELYLVGVFRTLDDIESKDAIPNFLQKKTGRKDPLLFSILREILNY 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NMD2 gene; Nmd2p protein; nonsense-mediated mRNA decay pathway; yeast; nonsense mutation; therapy; breast cancer; haemophila; polycystic kidney disease; Nieman-Pick disease; cystic denomatous polyposis coli; Fanconi's anaemia; neurofilbromatosis; hypercholesterolaemia; ornithine transcarbamylase deficiency; retinoblastoma; glycogen storage disease; McArdle disease; cancer; Tay-Sachs disease; Cowden disease; Milson disease; beta-thalassaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                  317 AKIIKREEMVNYFARLIDRIKTVCEV------VNLTNLHCILDFFCEFSEQSPCVL
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                                                                                                                                                                             197 LKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKETS
                                                                                                                                                                                                                                                                                                                                    Yeast Nmd2p involved in nonsense-mediated mRNA decay pathway
                                                          ----ICDIAREKVNK-AAVFEEED--FQSMTYGFKMANSVTDL
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                                                                                                                                                                                                               254 HKKV-NKLOREHOKCOIRTGKLRDEYVE-EYDKLLPIFIRFK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nonsense-mediated mRNA decay gene and protein - used to develop methods for inhibiting the decay pathway for producing heterologous or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nonsense-mediated mRNA decay; NMD2; Upf1p; inhibition.
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                                                                                                                                                                                                                                                                     This sequence represents Nmd2p, the protein encoded by the newly discovered NMD2 gene (see AAX25601) of Saccharomyces cerevisiae. NMD2 and discovered NMD2 gene (see AAX25601) of Saccharomyces cerevisiae. NMD2 named after its role in the nonsense-mediated mRNA decay pathway. A cterminal fragment of Nmd2p also binds to Upflp and, when overexpressed in a host cell, inhibits the function of Upflp, thereby inhibiting the nonsense-mediated mRNA decay pathway to methods of inhibiting the nonsense-mediated mRNA decay pathway to methods of inhibiting the nonsense-mediated mRNA decay pathway to would cause an increase in the transcript decay rate. Such stabilisation also relates to methods of inhibiting the transcript decay rate. Such stabilisation also allows increased translation from the transcript, and is therefore useful for the production of a recombinant protein. The invention also relates to methods of identifying molecules that inhibit the nonsense-mediated mRNA decay pathway, and the use of such molecules (e.g. the C-terminal fragment of Nmd2p or an antisense molecule) for treatment of disorders associated with nonsense mutations, such as breast cancer, polycystic kidney disease I and II. Niemann-Pick disease, adenomatous polyposis coli, cystic fibrosis, Fanconi's anaemia, haemophilia, hypercolommia, neurofibromatosis, ornithine transcript mannance afficiency actions in perceiphromatosis, ornithine transcripting and afficiency actions and antisense molecules is ornithine transcripting and afficiency actions and antisense molecules is ornithine transcripting and afficiency and antisense molecules is ornithine transcripting and afficiency and antisense molecules is ornithine transcripting and afficiency and antisense molecules is ornithine transcripting and antisense molecules and antisense molecules and antisense molecules and antisense molecules and antisense molecules and antisense molecules and antisense molecules and antisense molecules and antisense molecules and antisense molecules and antisense and antise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AKIIKREEMVNYFARLIDRIKTVCEV------VNLTNLHCILDFFCEFSEQSPCVL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 KRNTGFIKKLKKGFVKGSESSLLKDLSEASLEKYLSEIIVTTTECLLNVLNKNDDVIAAV 94
                                                                                                                                                                                            mRNA decay pathway genes and protein useful for treating breast cancer and cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deficiency, retinoblastoma, glycogen storage disease, McArdle disease,
cancer, Tay-Sachs disease, Cowden disease, Wilson disease or beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAMSAI-EMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITWLEGHSLAQTVFTCLYIHN------PDFIE-----DPAMKAFALGILK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ICDIAREKVNK-AAVFEEED--FQSMTYGFKMANSVTDL------RVTGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 LKDVEDDMORRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVLLTVLLAFTKKETS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3%; Score 127; DB 2; Li
17.6%; Pred. No. 0.014;
ive 124; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSNTNWV-------DITODFEEACRELKLGELL-
                                                                                                                                                                                                                                             Example 3; Fig 1A-C; 116pp; English.
               98WO-US022365.
                                             97US-00955472.
                                                                              (UYMA-) UNIV MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thalassemia (claimed)
                                                                                                                                             WPI; 1999-302756/25.
                                                                                                              He F, Jacobson AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1089 AA;
                                                                                                                                                              N-PSDB; AAX25601
               21-OCT-1998;
                                             21-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117;
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469
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s disease;
PVLSPKCYLYNNHQA 417
                                KDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDA 477
                                                                                                                                                                                                                                                  478 ALHTMLLKQEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFL 537
                                                                                                                                                                                                                                                                                                                517
                                                                                                                                                                                                                                                                                                                                                                           YAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREITMSQAYQNMCAGM 597
                                                                                                                                                                                                                                                                                                                                                                                                               -----LNKPEYKELMEKAY-------QLIKDKKNDRQLN--MNMKSALENITIL 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The nonsense-mediated mRNA decay pathway has an important role in the degradation of mRNA transcripts that contain a stop codon. The products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        upf3p; gene therapy; beta-thalassmäemia; cancer; polycystic kidney disease; Duchenne muscular dystrophy; Fanconi anaemia polycystic kidney disease; Duchenne muscular dystrophy; Fanconi anaemia haemophilia; hypercholesterolaemia; neurofilbromatosis; Tay-Sachs disease glycogen storage disease; cystic fibrosis; adenomatous polyposis coli; Cowden disease; Maple syrup urine disease; Wiscon disease; Niemann-Pick disease; Turcot syndrome; McArdle disease; Niemann-Pick disease; arthroise deficiency; antisense therapy; ribozyme.
                                                                                                                                                                                                                                                                                            -NKINVKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast; nonsense-mediated mRNA decay pathway; NMD2; UPF3; UPF1; upf1p;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Carboxy_terminal
/note= "Fragment is described in AAY98056"
SRSLLQTTFLVD--NKKVFGTHLMQDMVKD-ALRSFVDP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY98055 standard; protein; 1089 AA.
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                                                                                                                                                                                PEIVSEFINYLDNGFRS--QLHS-
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97US-00955472.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a gene without mutation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598 FKTMV 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-422078/
N-PSDB; AAA39450.
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of the UPP1 and UPP3 genes (proteins Upf1p and Upf3p, respectively) are essential components of this pathway. Mutations in these genes stabilise mENNA containing premature stop codons. The present sequence is the NWD2 gene protein from Saccharcomyces cerevisiae: NMG2p. The carboxy terminal of this protein from Saccharcomyces cerevisiae: NMG2p. The carboxy terminal consense-mediated mENNA decay pathway is a useful means of treating disorders caused by the presence of nonsense mutations, e.g. breast cancer, polycystic Kidney disease, Niemann-Pick disease, adenomatous polyposis coli, cystic fibrosis, Fanconi's anaemia, haemophilia, hypercholesterolaemia, neurofibromatosis, ornithine transcarbanylase deficiency, retinoblastoma, glycogen storage disease, McArdle disease, colorectal cancer, Tay-Sachs disease, Cowden disease, Wilson disease, colorectal cancer, Tay-Sachs disease, Cowden disease, Wilson disease, colorectal cancer, Tay-Sachs disease, Cowden disease, Purcot carcinoma, Li-Fraumeni syndrome, Maple syrup urine disease, Turcot syndrome or beta-thalassaemia. Antisense mENNA molecules complementary to the NMD2 gene may be used for antisense mena manipulated for ribozyme therapy of the above mentioned disorders: ribozymes designed to catalytically cleave nonsense-mediated mENNA decay pathway mENNAs e.g. NMD2 mENNA, can also be used to prevent translation and therefore expression of these mENNAs. 256 58 EAMSAI-EMMDPKWDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCL 116 193 156 -----ICDIAREKVNK-AAVFEEED--FQSMTYGFKMANSVTDL------RVTGM 196 AVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRY 316 317 AKIIKREEMVNYFARLIDRIKTVCEV------VNLTNLHCILDFFCEFSEQSPCVL 366 :: : |: | : | : | : | 335 QRLWENEDTRKFYEILPDISKTVEERQSSKTEKDSNVNSKNINL---FFTDL-EMADC-- 388 118 KDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDA 477 478 ALHTMILKQEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFL 537 538 YAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREITMSQAYQNMCAGM 597 -----PDFIE-----DPAMKAFALGILK- 155 296 AITLGEFFKLEIPELEGASNDDL-----KETA-----SPMITNQILPPN--- 334 94 194 KFKLGFTTTIATAFIKKFAPLFRDDDNSWDDLIYDSKLKGALQSLFKNFIDATFARATEL -----HDKLFGLF 35 KRNTGFIKKLKKGFVKGSESSLLKDLSEASLEKYLSEIIVTVTECLLNVLNKNDDVIAAV | :| : : : : : : | | | | | : : : | | | | | ELISGLHQRFTSPLLG-----QR 367 SRSLLQTTFLVD--NKKVFGTHLMQDMVKD-ALRSFVDP-----PVLSPKCYLYNNHQA Query Match 3.3%; Score 127; DB 3; Length 1089; Best Local Similarity 17.6%; Pred. No. 0.014; Matches 117; Conservative 124; Mismatches 202; Indels 222; Gaps 197 LKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKETS 254 HKKV-NKLQREHQKCQIRTGKLRDEYVE-BYDKLLPIRFK-----TS 24 KSNTNWV------DITQDFEEACRELKLGELL-ITWLEGHSLAQTVFTCLYIHN--Sequence 1089 AA; 117 389 à d g à a à g ð g ð g ò g à d à qq ð g

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34 QDFEEACRELKIGELLHDKLFGLFEAMSAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDG
                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                           WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                               Similarity
602
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559 YPPSV 563
                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                N-PSDB; AAS81522.
                                                                                                                                                                                                                                                                                                                  Sequence 1257 AA;
598 FKTMV
                                                                                             WO200175067-A2.
                                                                                                                                                                                       biodiversity.
                                                                                                                                                                             diagnostics,
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Best Local Simi
Matches 140;
                                                                                                       11-OCT-2001
                                          ABG17335;
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                       RESULT 14
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        원
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 116; Mismatches 246; Indels 264; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping, gene mapping; gene therapy, forensic, food supplement, medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynuclectide and encoded polypeptides, useful in
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                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #17326.
ABG17335 standard; protein; 1257 AA.
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23-AUG-2000; 2000US-00649167.
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23-AUG-2000; 2000US-00649167

(HYSE-) HYSEQ INC

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                                                  60 WDYVKRPNL-RLIGVPES-----DAENGTKLENTL-----QDIIQEDFPNLARQAN
                                                                                                                     VQIQEIQRTPQRYSSRRATPRHIIVRFTKVEMKQKMLRAA--REKDFKPTKIKRDKEGHY
                                                                                                                                                                                                                                                                                                                                                                   ----SRS----TTWKLNNNMLLNDYWVHNKMKAEIKMFFET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 QEQTWHSKASRRQEITKIRAELKEIETQKILQKINESRSWPFERINKIDRPLARLIKKKR
 RELREECRSLR-----SRRNQLEERVSAME--DEMNEMKREGKFREKRIKRNEQSLQEI
                              TIKIKDLILPELIGIMDICFCCLITWLEGHSLAQTVFTCLYIHNPDFIEDPAMKAFALGI
                                                                                                                                                     -TG----MLKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQ
                                                                                                                                                                                                               230 CLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNSLHHG-----I
                                                                                                                                                                                                                                             ------ISTLDRSTROKVNKDTQELNSALHQADLID-IYRTLHPKSTEYTFF
                                                                                                                                                                                                                                                                          QAQNDT-TKGDHPIMMGFEPLVNQRLLPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEV
                                                                                                                                                                                                                                                                                              VNLTNLHCILDFFCEFSEQSPCVLSRSLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVDP
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                                                                                                                                                                                  163 IMVKGSIQQEELTILNIYAPNTGAPRFIKQVLSDLQRDLDSHTLIMGDFNTP----
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food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                          --EKVNKAAVFEEEDFQS----
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this spatent did not appear in the printed specification, but was obtained in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
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87; Mismatches 201;
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550 GSQMAEERIMEEQQKGRSSKKTKK--KKKVRPLSREITMSQAYQNMCAGMFKTMVAFDMD 607

qa	
ò	608 GKVRKPKFELDSEQVRYEHRFAPFNSVMTPPPVHYLQFKEMSDLNKYSPPPQSPELYVAA 667
qq	465 GFTAEFYQ-RYKEELVPFLLKQFQSIEKEGILPNS 498
ζ	ENI PNPDHEVNRI LKVAKPNF
qa	499FYBASIILIPKPGRDTTKKENFRPMSLMNIDAKILNKILANGIQQHIK 546

Search completed: August 10, 2004, 21:50:11 Job time : 63 secs

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August 10, 2004, 21:52:08; Search time 50 Seconds (without alignments) 4598.592 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp:*

cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/DS06_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/NS08_PUBCOMB.pep:*

cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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ls: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVMKASVDDDDSGWELSMPE.....KVPPEFDFSAHKYFPVVKLV
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1291235 seqs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                       US-10-001-857-145
3849
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                      Run on:
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		Description	Sequence 145, App	Sequence 3, Appli	Sequence 146818,	Seguence 190465,	Sequence 220965,	Sequence 40, Appl	Sequence 2722, Ap	Sequence 55, Appl	Sequence 696, App	Sequence 7409, Ap	Sequence 7410, Ap	Sequence 65126, A	Sequence 64, Appl	Sequence 3, Appli	Sequence 40, Appl
		ID	US-10-001-857-145	US-10-467-433-3	US-10-437-963-146818	US-10-424-599-190465	US-10-424-599-220965	US-10-403-571-40	US-10-408-765A-2722	US-10-225-486-55	US-10-408-765A-696	US-10-335-977-7409	US-10-335-977-7410	US-10-425-114-65126	US-09-888-615-64	US-10-412-897-3	US-09-964-956-40
		DB	13	16	16	12	12	12	16	14	16	12	12	12	9	15	12
		Match Length DB ID	733	725	206	256	355	965	2419	191	191	696	972	745	3353	1441	1641
a)e	Query	Match I	100.0	98.3	15.5	8.4	5.4	3.6	3.5	3.3	3.3	3.3	3.3	3.1	3.1	3.0	3.0
		Score	3849	3783	595.5	322.5	206.5	139.5	136	127	127	127	127	121	119	116.5	116.5
	Result	No.		7	æ	4	2	9	7	8	6	10	11	12	13	14	15

Sequence 5, Appli	Sequence 285, App	23,		34,			79,		Sequence 52, Appl	Sequence 6744, Ap	Sequence 22080, A			2070	Sequence 175526,	Sequence 110215,	Sequence 3, Appli	Sequence 2, Appli	(1)	Sequence 5, Appli		Sequence 168, App	190,	6125	Sequence 191477,	142,	Ψ	3294	Sequence 12211, A
.3 US-10-017-216-5	.2 US-10-170-385-285		.3 US-10-002-769-14	3 US-10-024-623-34	4 US-10-154-419-46	4 US-10-154-419-84		.6 US-10-437-963-200109	L5 US-10-161-493-52	LS US-10-369-493-6744				L5 US-10-369-493-2070	16 US-10-437-963-175526	16 US-10-437-963-110215	US-09-742-096-3	L2 US-10-415-253-2	l3 US-10-041-856-3		L2 US-10-424-599-164683	L3 US-10-078-929-168	L4 US-10-078-770-190	L2 US-10-282-122A-61253	16 US-10-437-963-191477	L6 US-10-287-226-142	LS US-10-369-493-6734	L5 US-10-320-797-3294	9 US-09-815-242-12211
1641 1	736 1	633	1187 1	1187 3	1187 3	-		•	1191				1192	1957	•	1012	1786	1787	1332	1332	662	909	909	533	1321	1401	2427	794	981
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116.5	116	115	115	115	115	115	115	114.5	114.5	114.5	114	113.5	113.5	113.5	112	112	112	112	111.5	111.5	111	110	110	109.5	109.5	109.5	109.5	109	109
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 145, Application US/10001857
Publication No. US202020183500A1
GENERAL INFORMATION:
APPLICANT: Macina, Noberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
FILE REFERENCE: DEX-0273
CURRENT APPLICATION NUMBER: US/10/001,857
CURRENT FILING DATE: 2003-11-20
FRICK PROMER: 2003-11-20
CURRENT FILING DATE: 2003-11-20
FRIOR APPLICATION NUMBER: 60/252,054
FRIOR APPLICATION NUMBER: 60/252,054
FRIOR APPLICATION NUMBER: 5000-11-20
SUMMER OF SEQ ID NOS: 208
SUSTUMER PLACE PACENTIN VERSION 3.1
SEQ ID NO 145
LENGTH: 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 EGHSLAQTVFTCLYIHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFEEDFQSMTY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCLITWL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MYMKASVDDDDSGWELSMPEKMEKSNTNWVDITQDFEEACRELKLGELLHDKLFGLFEAM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVMKASVDDDDSGWELSMPEKMEKSNTNWVDITQDFEEACRELKLGELLHDKLFGLFEAM
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 733; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapien
US-10-001-857-145
US-10-001-857-145
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                                                                                                                                          241 RVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPINMGF 300
                                                                                                                                                                                                             EPLVNQRILPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEVVNLTNLHCILDFFCEFSE 360
                                                                                                                                                                                                                                                                 420
                                                                                                                                                                                                                                                                                                                                            480
                                                                                                                                                                                                                                                                                                                                                              TMLLKQEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFLYAW 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVAFDMDGKVRKPKFELDSEQVRYEHRFAPFNSVMTPPPVHYLQFKEMSDLNKYSPPPQS 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELYVAASKHFQQAKMILENIPNPDHEVNRILKVAKPNFVVWKLLAGGHKKESKVPPEFD 720
                                                                                                                                                                                                                                                                                                  QSPCVLSRSLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVDPPVLSPKCYLYNNHQAKDC 420
121 EGHSLAQTVFTCLYIHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFEEEDFQSMTY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                           TWITKQEPQRQHLACLGTWVLYHNIRIMIQYLLSGFELELYSWHEYYYIYWYLSEFLYAW
                                                                                                                                                                                        EPLVNQRIL PPTFPRYAKI IKREEMVNYFARLIDRIKTVCEVVNLTNLHCILDFFCEFSE
                                                                                                                                                                                                                                                                                                                                        IDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDAALH
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                                                                                                              RVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGF
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                                   GFKMANSVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFT
                                                                   GFKMANSVIDLRVIGMLKDVEDDMQRRVKSTRSRQGEERDPEVELEHOOCLAVFSRVKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CANT: LAL, Preeti G.; BAUGHN, Mariah R.;
CANT: YAO, Monique G.; CHAWLA, Nariaher K.;
CANT: ELLIOTT, Vicki S.; XU, Yuming,
CANT: ELLIOTT, Vicki S.; XU, Yuming,
CANT: HONCHELL, Cynthia D.; YUE, Henry,
CANT: ISON, Craig H.; LU, Dyung Ana M.;
CANT: ISON, Craig H.; LU, Dyung Ana M.;
CANT: THANGAVELO, Kavitha; SANJANWALA, Madhusudan M.;
CANT: THANGAVELO, Kavitha; SANJANWALA, Madhusudan M.;
CANT: THANGAVELO, Kavitha; SANJANWALA, Madhusudan M.;
CANT: TRAG, Y. Tom; RAWKUMAR, Jayalaxmi;
CANT: GRIFFIA, Jennifer A.; SWARNAKCR, Anita;
CANT: BURFORD, Neil; LEE, Ernestine A.;
CANT: LU, Yan, TRAN, Uyen K.;
CANT: MARQUIS, Joseph P.
OP INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFPLICANT: MARQUIS, JOSEPH P.;
AFPLICANT: MARQUIS, JOSEPH P.;
TITLE OF INVENTION: MOLECULES FOR DISEASE DE
FILE REFREENCE: FF CA999 USN.
CURRENT APPLICATION NUMBER: US/10/467,433
CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US 60/268,117
PRIOR PLILING DATE: 2002-02-08
PRIOR FILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-09
PRIOR PLILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10467433

Publication No. US20040087773A1

GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION;
APPLICANT: LAL, Preeti G.; BAUGHN, M
APPLICANT: ELLIOTT, Vicki S.; XU, YU
APPLICANT: ELLIOTT, Vicki S.; XU, YU
APPLICANT: HONCHELL, Cynthia D.; YUE
APPLICANT: HONCHELL, Cynthia D.; YUE
APPLICANT: ISON, Craig H.; LU, Dyung
APPLICANT: HAFALIA, April J.A.; GAND
APPLICANT: THANGAVELU, Kavitha; SANJ
APPLICANT: TANG, Y. TOM; RAMKUMAR, J.
APPLICANT: AZINZEL, Yalda; SAPENTANT:
APPLICANT: AZINZEL, Yalda; SAPENTANT:
APPLICANT: AZINZEL, Yalda; SAPENTANT:
APPLICANT: AZINZEL, Yalda; SAPENTANT:
APPLICANT: AZINZEL, Yalda; SAPENTANT:
APPLICANT: BURFORD, NGIL; LEE, ETDES
APPLICANT: HONCHELL, YALD, TEAN, UYEN K.;
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PRIOR FILING DATE: 2001-02-23

PRIOR PILING DATE: 2001-02-23

PRIOR PILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: US 60/274,486

PRIOR PILING DATE: 2001-03-09

PRIOR FILING DATE: 2001-03-09

PRIOR FILING DATE: 2001-11-28

PRIOR FILING DATE: 2001-11-28

PRIOR FILING DATE: 2002-01

NUMBER OF SEG ID NOS: 40

SOFTWARE: PERL PROGram

SEQ ID NO 3

LENGTH: 725

TYPE: PRT

ORGANISM: Homo sapiens

FATURE:

PRATURE:

OCHER INFORMATION: Incyte ID NO: 7111920CD1
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Shou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: 20/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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: | | :: | | | :| | 476 TRNVLPHENMCMRVSKQ-----LLVWTQEHTYWVAXRFLILGFELDLYSPSEYCMVY--
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                                                                                                                                                                                                                                                                   587 SQAYQNMCAGM-FKTMVAFDMDGKVR---KPKFELDSEQVRYEHRFAPFNSVMTPPPVHY
                                                                                                                                                                                                                                                                                                                                              555 LQCYVLLSEGLSMDFQAAFSQXIHINSHWNWKLEFIALRGRFIQHFDLLQKARLPEHITY
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                                                                                                                  533 LSEFLYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREIT---
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                                                                                                                                                                                                                                                                                                                                                                                                                         643 LQFKE-----MSDLNKYSPPPQSPELYVAASKHFQQAKMILENI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_143009C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          690 RILKVAKPNFVVMKLLAGGHKKESKVPPEFDFSAHKYFPV
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max
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LENGTH: 256
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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bradalt, Brad
APPLICANT: Bring and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 39-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 146818
TENGTH: 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVEDDMQRRVKSTRSR-----QG-BERDPEVELEHQQCLAVFSRVKFTRVLLTVLIA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V--GFDASLNSRLLSPAPPRAVKLLSWSDAIRYFEKLLRDLDIICSSPLDPVLENVLHFV 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EFVVQLGQLVINLLKILCTNTAWQRRKLGKSLQDWSTISIQ-LEFALKREFGE 475
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                               Sequence 146818, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bukharov, Andrey A.
                                                                          713 FSAHKYFPVVKLV
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US-10-437-963-146818
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89 AIKDGTIKIKDLTLPELIGIMDTCFCCLITWLEGHSLAQTVFTCLYIHNPDFIEDPAMKA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 ESLILLCSODDSKTA-----QATLKTALTSLVQMLKTCP-----HLSQSSVELLLRQ 437
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                                                                                                                                                                                                                                                                                                                                                 Indels 355;
                                                                                                                                                                                                                                                                                                  Query Match 3.6%; Score 139.5; DB 12; Length 965; Best Local Similarity 19.0%; Pred. No. 0.0013; Matches 182; Conservative 123; Mismatches 296; Indels 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 TDLRVTGMLKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSR--
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            CURRENT APPLICATION NUMBER: US/10/403,571
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: US 60/368,760
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 159
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LRLCVLKVTQLSEKHLEKİLNV----
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FILE REFERENCE: 01997/539002
                                                                                                                                                                                                                                 ORGANISM: Danio rerio
US-10-403-571-40
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                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Acvalic David K
APPLICANT: Shou Yihua
APPLICANT: Canou Yihua
APPLICANT: Canou Yihua
APPLICANT: Cav Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 220965
LENGTH: 355
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Publication No. US20040068763A1

GENERAL INFORMATION:
APPLICANT: Hopkins, Nancy
APPLICANT: American, Garegory
APPLICANT: American, Adam
APPLICANT: American, Adam
APPLICANT: American, Adam
APPLICANT: Sun, Zhoaxia
TITLE OF INVENTION: Developmental Mutations in Zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CTHER INFORMATION: Clone ID: PAT_MRT3847_41561C.1.pep
US-10-424-599-220965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(355)
OTHER INFORMATION: unsure at all Xaa locations
                   Sequence 220965, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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US-10-424-599-220965
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OY 645FKEMSDLNKYSPPPOSPELYVAASKHFQQAKMILENI 681	QY 682PNPDHEVNRI-LKVAKPNFVVMKLLAGGHKKESKVPPEFDFSAHKY 726	RESULT 7 US-10-408-765A-2722 US-10-408-765A-2722 Sequence 2722, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION: APPLICANT: Falsy, Soumitra S. APPLICANT: Falsy, Eoin D. APPLICANT: Zhang, Bing APPLICANT: Zhang, Bing APPLICANT: Applicant States W. APPLICANT: Applicant States W.	APPLICANT: APPLICANT: TITLE OF INV FILE REFERSE CURRENT APPL CURRENT FILE CURRENT FILE NUMBER OF SE SOFTWARE: FE	; LENGTH: 2419 ; TYPE: PRT ; ORCANISM: Homo sapiens US-10-408-765A-2722 Query Match Best Local Similarity 19.4%; Pred. No. 0.012; Matches 176; Conservative 141; Mismatches 333; Indels 288; Gaps 49;	GWELSMPEKMEKNINWVDITQDFEBACRELKLGELLHDKLFGLFEAMSIEM 6	QY         120 LEGHSLAQTVFTCLYIHNPDF1EDPAMKAFALGILKICDIAREKVNKA-AVF 170           bb          :         :	210 STRSRQGEBRDPEVELEHQCLAVFSRVKFTRVLLTVLIAFTKKETSAVA  1781 D-KAAVGGEEIQIRLAQFVEHWEKLKELARGKILESSLEYLQFRQNABEBEBANIN  260 EAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGFEPLVNQ  1837 EKNALAVRGCGDTLAATGSLLMKHBALENDFAVHFRVONVCAGEDILM-  1837 EKNALAVRGCGDTLAATGSLLMKHBALENDFAVHFRVONVCAGEDILM-	307 RILPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEVVNLTNLHCILDF-FCEFSES 36  1888

Qy         405 LSPKCVLYNNHQAKDCID-SFVTHCVRPFCSL 435           Db         326 LISPQLSPQLVRQQIAMAHLINQQIAVSRLLAHQHPQAINQPELNHPPIPRAKFPETNSS 385           Qy         436 IQHGHNRARQRDKLGHILBEFATLQDEFMTFYENRARKVDAALHTMLLKQBPQRQHLAC 495           n::::  :: : ::  ::  ::  ::  ::  ::  ::	RESULT 10  US-10-335-977-7409  US-10-335-977-7409  Sequence 7409, D20040052799A1  Publication No. US20040052799A1  Publication No. US20040052799A1  Publication No. US20040052799A1  Publication No. US20040052799A1  PUBLICATION NUCLEIC CAID AND AMINO ACID SEQUENCES  RELATING TO HELICOBACTER PULORI FOR INGRESCES: 10031  CORRESPONDENCE ADDRESS: 10031  ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: AD
QY 405 LSPKCYLYNNHQAKDCID-SFVTHCVRPFCSL 435  Db 326 LSPQLSPQLVRQQIAMAHLINQQIAVSRLLAHQHPQAINQQFLNHPPIPRAVKPBPTNSS 385  QY 436 IQIHGHNRARQRBKLGHILBEFATLQDEFMTFYFNRAEKVDAALHTMLLKQEPQRQHLAC 495  ::::	PRESULT 9  103-10-408-762A-696  103-10-408-762A-696  104-10-408-762A-696  105-10-408-762A-696  105-10-408-762A-696  105-10-408-762A-696  105-10-408-762A-696  105-10-408-762A-696  105-10-408-762A-696  105-10-408-762A-696  105-10-408-762A-696  105-10-408-762A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696  105-10-408-765A-696

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SOFTWARE: UNIX
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                                                                                                                                                          Gaps 37;
                                                                                                                                                                                                                                                                                                  -----ECVYALHK 100
                                                                                                                                                                                                                                                                                                                                    -IHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFEEEDFQSMTYGFKMANSVTDLRV 193
                                                                                                                                                                                                                                                                                                                                                                      ------ 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --HNLIYALD---SKKAFDCALVKSISVASVGESDEYFLELKEANKKQNEATINYTTLEN 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----RIKTVCEVVNLTNLHCILDFFCEFSEQSPCVLSRSLLQTTFLVDNKKVFGTHLMQ 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D----MVKDALRSFVD-----PPVLSPKCYLYNNHQAKDCIDSFVTHCVRP----FC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAE----KVDAALHTMLLKQEPQ 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 ROHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFLYAW----LMSTL 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LILKEKEKLLSFDSDL----RFIFSQWALQE---GWDNPNVMTIC 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SNÍTKLÓGIGRGERLAVNDKGERITKEHADFDFVNELVVIVPOVEGDFVG 550
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                                                                                                                                                                                                                                                              83 VLNFEQAIKDGTIKIKDLTLPELIGIMDT----CFCCLITWLEGHSLAQTVFTCLY---- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NHKCCVLVMTFSAFNKEKNTINQSCLEN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LIAFTKKETSAVAEAQKLMV------QAADLLSAIHNSLHHGIQAQNDTTK 291
                                                                                                                                                                                                              551 AIQQEISEHSLIKQVFSAEELEKSGMVKKGYYGVLFETLEGLGFGEKTDDENFKLTLNQ-
                                                                                                                     Query Match 3.3%; Score 127; DB 12; Length 969; Best Local Similarity 17.3%; Pred. No. 0.021; Matches 143; Conservative 125; Mismatches 271; Indels 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    676 MILENIPUPDHEVNRILKVAKPNFVVMKLLAGGHKKESKVPPEFD 720
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                                                                                                                                                                                         35 DFEEACRELKLGELLHDKLFGLFEAMSAIEMMDPKMDAGMIGNQV-
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                                                                                                                                                                                                                                                                                             57 NLRSKOKITOGSVGINOSLNCDI--LMETGTGKTFCFL
                             NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...969
SEQUENCE DESCRIPTION: SEQ ID NO: 7409:
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                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
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----ESYEDVERFILAS----
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                                                                                  US-10-335-977-7409
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US-10-335-977-7410 ; Sequence 7410, Application US/10335977 ; Sequence INO US20040052799A1 ; GENERAL INFORMATION:

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60 NLRSKQXITQGSVGINQSLNCDI--LMETGTGKTFCFL------ECVYALHK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 NYHLSKFIVLAPSNAIKLGVLKSIEITRE--------FFKSEYSNTHL-- 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 VLNFEQAIKDGTIKIKDLTLPELIGIMDT----CFCCLITWLEGHSLAQTVFTCLY---- 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LIAFTKKETSAVAEAQKLMV------QAADLLSAIHNSLHHGIQAQNDTTK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNLFNGAKSYMOALASMRPIVIMDEPHRFLGDKTKKYLEQLNAL-ITLRFGATFKDDY--
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APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 3.3%; Score 127; DB 12; Length 972; Local Similarity 17.3%; Pred. No. 0.021; es 143; Conservative 125; Mismatches 271; Indels 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 DFEBACRELKLGELLHDKLFGLFBAMSAIEMMDPKMDAGMIGNQV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...972
; SEQUENCE DESCRIPTION: SEQ ID NO: 7410:
US-10-335-977-7410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36, 207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAT (617) 742-4214
INFORMATION FOR SEQ ID NO: 7410:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              4.0
                                                                                                                                                                             ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT
                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 972 amino acids TYPE: amino acid
                                                                                                                          SEQUENCES: 10031
                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                    NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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159 KSQVEALEDALDV-----EDLEADKRPEDLMLSFVSGEKGKDRSDKEVVTPWFKFLWET 212
                                                                                                                              213 YRTVLEILRNNSKLEALYAMAAHRAFQFCKQYKRTTEFRRLCEIIRNHLANLNKYRDQRD 272
                                                                                                                                                                                                                     ---RPDLTAPESLQLYLDTRVEQLKVATE-LCLWQEAFR-----SVEDIHGLMSMVK- 320
                                                                                                                                                                                                                                                                                                   ----KMPKPSILVVYYAKLTEIFWVSDSHLYHAYAWLKLFNLQKNYNKNLSQKDLQLIA 375
                                                                                                                                                                                                                                                                                                                                               555 EERIME-----EQQKGRSSKKTKKKKVRPLSREITMSQAYQNMCAGMFKTMVAFDMD 607
                                                                                                                                                                                                                                                                                                                                                                                                                         -----VRKPKFELDSEQVR----YEHRFAPFNSVMTPPPVHYLQFK 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---C-----VRPFCSLIQIHGHNRARQRDKLG
                                                                                                                                                                                   452 HILEEFATLQDEFMTFYFNRAEKVDAALHTMLLKQEPQRQHLACLGTWVLYHNLRIMIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            647 EMSDL-NKYSPPPQSPEL---YVAASKH-----FQQAKMILEN-----IPNPD-
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                                                                                                                                                                                                                                                                 LLSGFELELYSMHEYYY----IYWYLSEFL---YAWLM-----STLSRADGSQMA
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                     -DPPVLSP-
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larity 19.3%; Pred. No. 0.89;
Conservative 99; Mismatches 235;
                     -VKDALRSFV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SICHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 2001-06-26
PRIOR PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
                                                                                                 410 Y----LYNNHQAKDCIDSFVTH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 64, Application US/0988615; Patent No. US2/020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::
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                     LLQTTFLVDNKKVFGTHLMQDM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
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Best Local Simi
Matches 124;
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US-09-888-615-64
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Serven E
APPLICANT: Screen, Serven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 65126
IENGTH: 745
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                                                                                                                                                                                                                                          490 RQHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFLYAW----LMSTL 545
                                                                                                                                                                                                                                                                          455 VQVIA-----LILKEKEKLLSFDSDL----RFIFSCWALQE---GWDNPNVMTIC 497
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                                                                                                                                                              434 SLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAE----KVDAALHTMLLKQEPQ 489
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----RIKTVCEVVNLTNLHCILDFFCEFSEQSPCVLSRSLLQTTFLVDNKKVFGTHLMQ 389
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                                                                                                       353 GEQEVMLKEAIKSHFEREEGLFKKGIKALCMVFING-----VNSYLSENEKPAKLALLFE
                         297 KIQSVKVKTHDNLGALTHISALEDYIVEKITKTEL---RFLNGFNLLLDQKEPF-SHLLE
                                                                              390 D----MVKDALRSFVD-----PPVLSPKCYLYNNHOAKDCIDSFVTHCVRP----FC
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US-10-425-114-65126
                                                                                                                                                                                                                                                                                                                            546 SRADGSQMAEERIMEEQQKGRSSKKTKKKKKVR-
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Publication No. US20040034888A1
GENERAL INFORMATION:
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US-10-425-114-65126
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APPLICANT: Leach, Martin D
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: No. US20040043926Alel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/09/964,956
CURRENT FILING DATE: 2001-09-26
  283 TRLREVSLEHEB-----QKLELKRQLTELQLSLQERESQLTA------LQAA--RAALES 329
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                                                                                        218 ERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHN
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691 LQKTRIELRSAREEAAHRKATDHPHPSTPATARQQIAMSAIVRSPEHQPSAMSLLAPPSS
                                                               -VTGMLKDVEDDMQR---RVKSTRSR--QGE
                                                                                                                                                                                                                                                                                                                        337 KTVCEVVN--LINLHCILDFFCEFSEQSPCVLSRSLLQTTFLVDNKKVFGTHLMQDMVKD
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                                                                                                                                                                                                                                                                                330 OLROAKTELEETTAEAEEEIO-----
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Burgess, Catherine E
Padigaru, Muralidhara
Kekuda, Ramesh
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Bllerman, Karen
Grosse, William M
Alsobrook II, John P
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179 EAHEKGKILSEQKAMINAM-
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                                                             175 FQSMTYGFKMANSVTDLR-
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                                      215 QGEERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKE-TSAVAEAQK--LMVQAADL
                                                                 2873 LHTLVPFLQHNHCTYHH-----SNIPMSLGPYFPCRENIKLIGGKSNIRPPRPEL
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                                                                                                                                                                                                              ---TFPRYAKIIKREEMVNYFARLIDRIKTVCEVVNLTNLHCILDFFCE-FSEQSPCVLS
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                                                                                                                            LSAI -----HNSLHHGIQAQNDTTKGDHPIMMG--FEPLVNQRLL------PP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.0%; Score 116.5; DB 15; Length Best Local Similarity 19.0%; Pred. No. 0.4; Matches 150; Conservative 132; Mismatches 316; Indels
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; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENC; TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020; FILE REPERENCE: D0193 NP; CURRENT APPLICATION NUMBER: US/10/412,897; CURRENT FILING DATE: 2003-04-11; PRIOR PILING DATE: 2002-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.2
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ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/235,631
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PRIOR FILING DATE: 2000-09-27
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PRIOR PLING DATE: 2001-03-17
PRIOR PLING DATE: 2001-03-17
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Query Match 3.0%; Score 116.5; DB 12; Length 1641; Best Local Similarity 19.0%; Pred. No. 0.5; Matches 150; Conservative 132; Mismatches 316; Indels 193; Gaps 39;

273 EKAVKASTEATELLONIROAKERAEREL---EKLHNREDSSEGIKKKLVEAEELEEKHRE 329 379 BAHEKGKILSBQKAMINAM------DSKIRSLEQRIVELSE-ANKLAANSSLFTQRN 428 :: :::|| :: || : || : |
429 MKA-----QEBMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKSRLLELE 482 278 SLHHG-IQAQNDTIKGDHPIMMGFEPLVNQRLLPPIFPRYAKIIKREEMVNYFARLIDRI 336 -----ALTAHRDEI----QRKFDAL 566 ALRSFVD---PPVLSPKCYLYNNHQAKDCIDSFVTHCVRPFCSLIQIHGH--NRARQ--- 446 614 -LRSEVDHILRREITEREMQLISQKQTMEALKTITCTMLEEQVLDLEALNDELLEKERÖWEA 672 447 -RDKLGHILBEFATLQDEFMTFYFNRABKVDAALHTMLLKQEPQRQHLACLGTWVLYHNL 505 GMIGNQ-----VNRKVLNFEQAIK--DGTIKIKDLTLPELIGIMDTCFCCLITWLEGH-- 123 -----SLAQTVFTCLYIHNPDFIEDPAMKAFALGILKICDIAREKVNKAAVFEEED 174 175 FQSMTYGFKMANSVTDLR------VTGMLKDVEDDMQR---RVKSTRSR--QGE 217 218 ERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHN 277 KTVCEVVN---LTNLHCILDFFCEFSEQSPCVLSRSLLQTTFLVDNKKVFGTHLMQDMVKD 394 483 TRLREVSLEHEE-----QKLELKRQLTELQLSLQERESQLTA-----LQAA--RAALES 20 EKMEKSNINWVDITQDF----EEACRELKLGELLH---DKLFGLFEAMSAIEMMDPKMDA 530 QLRQAKTELBETTAEAEEIQ---337 395 73 124 g g g qq 8. qq g ò PP 8 qq à ð à δ  $\delta$ 

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Search completed: August 10, 2004, 21:57:23 Job time : 54 secs

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7	Sequence 2, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 31, Appl	Sequence 11, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 15754, A	Sequence 115, App	Sequence 27, Appl	Sequence 1, Appli	Seguence 13, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli
US-09-080-897-2	US-09-323-735-2	US-08-899-595-3	US-09-112-450-4	US-09-419-291A-4	US-09-595-684B-31	US-09-914-259-11	US-08-514-975B-2	PCT-US95-12507-2	US-09-866-108A-15754	US-09-588-995A-115	US-09-180-422B-27	US-09-108-006C-1	US-08-999-774A-13	US-08-450-332-2	US-08-637-640-2	US-09-004-406C-2	US-08-328-254-6
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101.5	101.5	101.5	101.5	101.5	101.5	101.5	100.5	100.5	66	98.5	98.5	98.5	98	86	98	98	97.5
28	29	3.0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: Feng, He
APPLICANT: Feng, He
APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: HE ABSENCE OF NONSENSE-MEDIATED WRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300 FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEFAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              Sequence 2, Application US/08375300 Patent No. 5679566
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fasse, J. P. REGISTRATION NUMBER: 32,983
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Matches 117; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                      ---DPAMKAFALGILK- 155
                                                                                                                                                                                                          -RVTGM 196
                                                                                                                                                                                                                                                                                                                                                                                                     AVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGFEPLVNQRLLPPTFPRY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                       317 AKIIKREEMVNYFARLIDRIKTVCEV------VNLTNLHCILDFFCEFSEQSPCVL 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 KDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDBFMTFYFNRAEKVDA 477
                                                                                                                                                                                                                                  478 ALHTMILKQEPORQHLACLGTWVLYHNIRIMIQYLLSGFELELYSMHEYYYIYWYLSEFL
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Patent No. 601700
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Patent No. 6
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BIISGLHQRFNGRFTSPLLG-----AFLQAFENPSVDIES-ERDEL-
                                                                                                                                                                                                     ----ICDIAREKVNK-AAVFEEED--FQSMTYGFKMANSVTDL
                                                                                                      --PDFIE---
                                                                                                                                                                                                                                                                                                                                                      254 HKKV-NKLOREHOKCOIRTGKLRDEYVE-EYDKLLPIFIRFK-
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FastSEQ for Windows Version 2.0b
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441 PEIVSEFINYLDNGFRS--OLHS-----
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225 Franklin Street
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/955,472
FILING DATE:
                                                                                                   ITWLEGHSLAQTVFTCLYIHN-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ZIP: 02110-2804
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US-09-177-431-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 KFKLGFTTTIATAFIKKFAPLFRDDDNSWDDLIYDSKLKGALQSLFKNFIDATFARATEL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 AITLGEFFKLEIPELEGASNDDL-----KETA-----SPMITNQILPPN---- 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                        94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 LKDVEDDMQRRVKSTRSRQGEERDPEVELEHQQCLAVFSRVKFTRVLLITVLIAFTKKETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 SRSLLQTTFLVD--NKKVFGTHLMQDMVKD-ALRSFVDP-----PVLSPKCYLYNNHQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 KDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDA
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                                                                                                                                                                                                                                                                                                                  Length 1089;
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BIISGLHQRFNGRFTSPLLG-----AFLQAFENPSVDIES-ERDEL-
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                                                                                                                                                                                                                                                                                                                Score 127; DB 3; L
Pred. No. 0.0033;
I; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                               24 KSNTNWV------DITQDFEEACRELKLGELL-
                                            07917/050001
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NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 0791'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9806
TELEX: 20154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                      Conservative 124;
                                                                                                                                                                                                                                                                                                                3.3%;
                                                                                                                                                                                                                    / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-09-177-431-2
                                                                                                                                                                                                                                                                                                                                   Similarity
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PCT-US95-16930-2
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Best Local (
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VQAADL-----LSAIHNSLHHGIQAQNDTTKG-DHPIMMGFEPLVNQR-----LLPPT 312
                                389 -----KDIIDDLSNRYWSSYLDNKATRNKILKFFMETQDWSKLPVYS-RFIATNSKYM 440
                                                                                     418 KDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQDEFMTFYFNRAEKVDA 477
                                                                                                                                                                                                                                                                                                  367 SRSILLQTTFLVD--NKKVFGTHLMQDMVKD-ALRSFVDP-----PVLSPKCYLYNNHQA 417
                                                                                                                                  ------ NKINVKNI 469
                                                                                                                                                                                                                                                                    538 YAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKKRPLSREITMSQAYQNMCAGM 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 DDDDSGWELSMPEKMEKSNT----NWVDITQDFEEACRELKLGELLHDKLFGLFEAMSA
                                                                                                                                                                                478 ALHTMLLKQEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFL
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.9%; Score 113.5; DB 4; Length 1279; Best Local Similarity 20.3%; Pred. No. 0.092; Matches 155; Conservative 125; Mismatches 291; Indels 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6379941e1 motor proteins and methods for
TITLE OF INVENTION: No. 6379941e1 motor proteins and methods for
TITLE OF INVENTION: No. 6379941e1 motor proteins and methods for
TITLE REPERBUCE: 1031
CURRENT APPLICATION NUMBER: US/09/724,517
PRIOR APPLICATION NUMBER: US/09/641,807
PRIOR APPLICATION NUMBER: US/09/641,807
PRIOR FILLING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                 441 PEIVSEFINYLDNGFRS--QLHS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
COATION: (409)...(436)
COTHER INFORMATION: Xaa = any amino acid
US-09-724-517-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09724517
Patent No. 6379941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 EAMSAI-EMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIKIKDLTLPELIGIMDTCFCCL 116
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3.3%; Score 127; DB 5; Length 1089;
Best Local Similarity 17.6%; Pred. No. 0.0033;
Matches 117; Conservative 124; Mismatches 202; Indels 222;
         UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: The PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                  HETEROLOGOUS POLYBEPTIDE
PRODUCTION IN THE ABSENCE OF
NONSENSE-MEDIATED MRNA DECAY
FUNCTION
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                                                                                                                                                                3: Fish & Richardson
225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046WO1
TELECOMMULCATION:
TELEPHONE: (617)542-5070
TELEPHONE: (617)542-8906
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1089 amino acids
                       TITLE OF INVENTION: HETTILE OF INVENTION: PROJ
TITLE OF INVENTION: NON:
TITLE OF INVENTION: FUN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                     STREET:
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PKAEDLDACNLKRRKGSFGSIDH-LQKLDEQKKWLDEEVEKVLNQRQELEELEADL	Db 682 RKKMDAAKK	-KKLASLSIQNEKRA 716
313 FPRYAKIIKKBEMYNYFARLIDRIKTYCEVVNLTNLHCILDFFCEFSEGSPCVLS 367     :   :   : :   : :   : :   :   :   828 KKREAIVSKKEAILQEKSHLENKKLRSSQALNTDSLKISTRINLLEQELSEKN 880	QY 221 PEVELEHQQCLAVFSRVKFTRVLLTVLJAFTKKETSAVAEAQKLM	2KLM 265          LKTGOEEGLK 772
368 RSLLQTTFLVDNKKVFGTHLMQDNVKDALRSFVDPPVLSPKCYLYNN 414	VQAADL :     PKAEDLDACNLK	
-YFN 47     RYFN 99	313	CVLS
471 RAEKVDAALHTMLLKOEPQRQHLACLGTWVLYHNLRIMIQYLLSGFELE 519 : :       : : :   997 KVVNLREAERKQQLYNEEMKWKVLERDNMVRELESALDHLKLQCDRRLTLQQKEHEQKMQ 1056	RSLLQTTFLVDNKKVFGTHLMQDMVKDALRSFVDPP 	LYNN      EEG
520 LYSNHEYYXIYWYLSELYAWLMSTL-SRADGSQWAEERIMEEQQKGRSSKKTKKKKVR 578 1057 LLLHHFKEQDGGGIMETFKTYEDKIQQLEKDLYFYKKTSRDHKKKLKELVGE 1108	Qy 415 HQAKDCIDSFVTHCVRPFCSLIQIHGHNRARQRDKLGHILEEFATLQD-EFWTFYFN	YEN     FRYEN
579 PLSREITMSQAYQNMCAGMFKTMVAFDMDGKVRKFKFELDSE 620 	Qy 471 RAEKVDAALHTMLLKQEPQRQHLACLGTWULYHNIRIMIQYLLSGFELE : :	QYLLSGFELE 519   ::: QXKEHBQKMQ 1056
621QVRYEHRFAPFNSVMTPPPVHYLQFKEMSDLNKYS 655   :  :  :  :  :  :  :  :  :  :  :  :  :	QY 520 LYSMHEYYXIYWYLSEFLYAWLMSTL-SRADGSQMAEBRIMBEQQKGRSSKKTYKKKKKYR 	KKTKKKKVR 578     -  KKKLKELVGE 1108
US-09-641-807A-2 US-09-641-807A-2 Sequence 2, Application US/09641807A Patent No. 6440731 GENERAL INFORMATION: A APPLICANT: Bereaud, Christophe APPLICANT: Freedman, Richard TITLE OF INVENTION: No. 6440731e1 motor proteins and methods for	Qy 579 PLSREITMSQAYQNMCAGMFKTMVAEDMDGKVRKPKFELDSE	-ELDSB 620  :   REMDSSASSLRTQ 1167
VENTION: their use THE: 1031 LICATION NUMBER: US/09/641,807A LING DATE: 2000-08-17 EAGL ID NOS: 4100-08-17 TastesQ for Windows Version 4.0	RESULT 6 US-09-723-096-2 ; Sequence 2, Application US/09723096 ; Patent No. 6448026 ; GENERAL INFORMATION: APPLICANT: Herand, Christonhe	
	; APPLICANT: Freedman, Richard ; TITLE OF INVENTION: No. 6448026el motor proteins and methods ; TITLE OF INVENTION: their use ; FILE REFERENCE: 1031	for
FEATURE: NAME/KXY: VARIANT LOCATION: (409)(446) OTHER INFORMATION: Xaa = any amino acid -09-641-807A-2		
Query Match 2.9%; Score 113.5; DB 4; Length 1279; Best Local Similarity 20.3%; Pred. No. 0.092; Matches 155; Conservative 125; Mismatches 291; Indels 191; Gaps 39;	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2 ; LENGTH: 1279 ; TYPE: PRT	
8 DDDDSGWELSWPEKMEKSNTNWYDITQDFEBACRELKLGELLHDKLFGLFEAMSA 62     :	; PEATURE: ; FEATURE: ; NAME/KEY: VARIANT ; LOCATION: (409) (436) ; OTHER INFORMATION: Xaa = any amino acid	
INIKMKEDLIKELIKTGNDA IEDPAMKAFALGILKICDIA	Query Match 2.9%; Score 113.5; DB 4; Length 1 Best Local Similarity 20.3%; Pred. No. 0.092; Matches 155; Conservative 125; Mismatches 291; Indels	1279; 191; Gaps 39;
629 KSVSKQYSLKVŤKĽEHDAEQAKVEĽIEŤQKQLQELENKĎ-LSĎVÁMKVKLQKEF 681 161 REKVNKAAVFEEEDFQSMTYGFKMANSVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEERD 220  : ::      :	QY 8 DDDDSGWELSMPEKMEKSNTNWVDITQDFEEACRELKLGELLHDKLFGLFEAMSA 	LFGLFEAMSA 62 TQKSD 568

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                                                                                                                                                     PEVE--LEHQQCLAVFSRVKFTRVL-----LTVLIAFTKKETSAVAEAQ-----KLM 265
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                                                                                                                                                                                                                                 717 NELEQSVDHMK----YQKIQLQRKLREENEKRKQLDAVIKRDQQKIKEIQLKTGQEEGLK 772
                                                                                                                                                                                                                                                                    VQAADL-----LSAIHNSLHHGIQAQNDTTKG-DHPIMMGFEPLVNQR-----LLPPT 312
                                                                                                                                                                                                                                                                                                                                      313 FPRYAKIIKREEMVNYFAKLIDRIKTVCEVVNLTNLHC----ILDFFCEFSEQSPCVLS 367
                                                                                                                                                                                                                                                                                                                                                                                                        RSLLQTTFLVDNKKVFGTHLMQDMVKDAL---RSFVDPP-----VLSPK-----CYLYNN 414
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APPLICANT: DRUILHE, PIERRE
APPLICANT: DRUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT APPLICATION NUMBER: DCT/FR96/00894
BARLIER APPLICATION NUMBER: PCT/FR96/00894
BARLIER APPLICATION NUMBER: F 95/07007
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PALENTIN Ver. 2.0
                   --MDTCFCCLITWLEGHS----LAQTVFTCLYIHNPDFIEDPAMKAFALGILKICDIA
                                                                                                                                                                                                                                                                                                      PKAEDLDACNLKRRKGSFGSIDH-LOKLDEOKKWLDEEV----EKVLNORQELEELEADL
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                                                                                                                                 REKVNKAAVFEEEDFQSMTYGFKMANSVTDLRVTGMLKDVEDDMQRRVKSTRSRQGEERD
                                                                                               KSVSKQYSLKVTKLEHDAEQAKVELIETQKQLQELENKD-LSDVAMK-----VKLQKEF
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence:Polypeptide
US-08-973-462-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---QVRYEH--RFAPFNSVMTPPPVHYL--QFKEMSDLNKYS 655
IEMMDPKMDAGMIGNQVN-RKVLNFEQAIKDGTIKIKDLT-
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                                                                                                            Gaps
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                                                                                                            242;
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APPLICANT: Cohen, Lucy
APPLICANT: Baeuerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 2
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
STREET: 75 DENISE DRIVE
STATE: CALIFORNIA
COUNTRY: USA
     Length 1786
Query Match 2.9%; Score 112; DD 3; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; DD 2; D
                                                                                                                                                                                                             17 SMPEKMEKSNTNWVDITQDFEEACRELKLGELLH----DKLF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-08-971-244-2
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FILING DATE
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                                                                                                                                                                                                                                                                                                            COUNTRY:
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US-09-286-891-2
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                                                                                                                                                                                                                                                                                                                                                                                                       70 MDAGMIGNOVN-----RKVLNFEQAIKDGTIKIKD-----LTLP-----BLIGIMDTCFCCL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LYIHNPDFIEDPAMKAFALGILKICDIAREKVNK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      730 RKWLD-KLMFKEAFECMRKLRINLNPIYDHNP------KVF-LGNVETFIKQIDSVNH 779
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        SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,244
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONMAN, RICHARD A
REGISTRATION NUMBER: T97-011
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                         2.9%; Score 111.5; DB 2; llarity 18.7%; Pred. No. 0.16; Conservative 110; Mismatches 252;
PC-DOS/MS-DOS
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                                                                                                                                                                                                             L.S.IH: 1332 amino acids
TYPE: amino acids
TOPOLOGY: 1:--
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OPERATING SYSTEM:
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Best Local
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                                  716
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661 PELYVAASKHFQQAKMILENIPNPDHEVNRILKVAKPNFVVMKLLAGGHKKESKVP
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                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Cohen, Lucy
APPLICANT: Cohen, Lucy
APPLICANT: Cohen, Lucy
APPLICANT: Will Beauerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.9%; Score 111.5; DB 3; Best Local Similarity 18.7%; Pred. No. 0.16; Matches 145; Conservative 110; Mismatches 252;
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APPLICATION NUMBER: US/09/286,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/971,244
FILING DATE:
ATTORNAY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                  US-09-286-891-2
; Sequence 2, Application US/09286891
; Patent No. 6172195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                               PEIWILI---YOO-
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 75 CL...
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us-10-001-857-145.rai

	RESULT 11 US-09-723-820-8  i Sequence 8, Application US/09723820  j Patent No. 6468760  GENERAL INFORMATION:  APPLICANT: Nislow, Corey  APPLICANT: Baraud, Christophe  TITLE OF INVENTION: Antifungal Assay  FILE REFERENCE: 1015  CURRENT APPLICATION NUMBER: US/09/723,820  CURRENT FILING DATE: 2000-11-28  PRIOR FILING DATE: 2000-04-03  NUMBER OF SEQ ID NOS: 10  SEQ ID NO 8  LENGTH: 1066  TYPE: PRT  CORGANISM: Drosophila melanogaster  US-09-723-820-8	Query Match  2.8%; Score 109.5; DB 4; Length 1066;  Best Local Similarity 19.7%; Pred. No. 0.17;  Matches 85; Conservative 80; Mismatches 168; Indels 99; Gaps 21;  Qy 122 GH-SLAQTVFTCLXIHNDDFIEDPAMKAFALGILKI-CDIAREKVNKAA 168  Db 336 GHKDIEBTLSTLEYAHRAKNIQNKPEVNQKLTKKTVLKEYTEEIDKLKRDIMAARDKNGI 395  Qy 169 VFEEDFGSMTYGFKMANSVTDLRVTGMLKDVEDDMQRRVK-STRSRQGEERDPEVELE 226  Db 396 YLABETYGEITLKLESQNREINERML-LLKALKDELQNKEKIFSEVSMSLUVEKTGEKKK 454  Qy 227 HQQCLAVFSRVKFTRVLLTVULAFTKKETSAVAEAQKLMVQAADILSAI 275	Db 455 EBLINTKGTLLTKKVLTKTRRYKEKKELVASHMKTEQVLTTGAGELLA-AADLATD 513  QY 276 HNSLHHGIQAQNDTTKGDHPIMMGEBLVAKIIKREE 324  E 14 THQLHGIQAQNDTTKGDHPIMMGEBLVAKIIKREE 324  S14 THQLHGTLERRELDEKIRRSCDQFKDRMQDNLEMIGGSLNLYQDQQALKEQLSQE 570  QY 325 MVNYFARLIDRIKTRCC-EVVLTNLH-CLIDFFCEFSEQSPCVLSRSLL 371  E 1
	Oy 515		Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --FVIHCVRPFCSLIQIHGHNRARQRDKLGHI----LEEFATLQDEFWTFYPNR--AEKV 475
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19.7%; Pred. No. 0.17;
ive 80; Mismatches 168; Indels 99;
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APPLICANT: Baraud, Christophe
TITLE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/10/270,085
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/723,820
PRIOR APPLICATION NUMBER: US/09/723,820
PRIOR APPLICATION NUMBER: US/09/723,820
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
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Iwamatsu, Akihiro
Makano, Takeshi
Ito, Masaaki
Takahashi, No. 5906819uaki
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Patent No. 5906819
GENERAL INFORMATION:
APPLICANT: Kalbuchi, Kozo
APPLICANT: Iwamatsu, Akihiro
APPLICANT: Inkanatsu, Akihiro
APPLICANT: Iro, Masaaki
APPLICANT: Takahashi, No. 5906819u
                                                                     ; Sequence 8, Application US/10270085; Patent No. 6627408
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DALLESMMMQME 734
                                                                                                                                                                          APPLICANT: Nislow, Corey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1066
RESULT 12
US-10-270-085-8
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US-08-685-576-1
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Best Local
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218 ERDPEVELEHQQCLAVFSRVKFTRVLLTVLIAFTKKETSAVAEAQKLMVQAADLLSAIHN 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 KVFGTHLMQDMVKDALRSFVDPPVLSPKCYLYNNHQAKDCIDSFVTHCVRPFCSLIQIHG 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      847 ELRKERQDADGQMKE----LQDQLEABQYFSTLYKTQVRELKECEBKTKLCKELQQKKQ 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 LACLGTWVLYHNLRIMIQYLLSGFELELYSMHEYYYIYWYLSEFLYAWLMSTLSRADGSQ 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --HLLEMKMSLEKONA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 HNRARQRDKIGHILEEFATLQDE----FMTFYFN--RAEKVDAALHTMLLKQEPQRQH 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 IAREKVNKAAVFEEEDFQSMTYGFKMANSVTDLRVTGMLKDVEDDMQRRVK-STRSRQGE
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RHO TARGET PROTEIN RHO-KINASE
                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,576
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
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                                                                   E: Foley & Lardner
3000 K Street, N.W., Suite
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PRIOR APPLICATION NUMBER: UP 7-325129
FILING DATE: 20-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 8-17150
FILING DATE: 05-JAN-1996
PRIOR APPLICATION NUMBER: UP 8-131206
FILING DATE: 26-APR-1996
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                             ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 16 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 1388 amino acids
amino acid
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                     NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                               Washington
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Best Local Similarity
Matches 87; Conserv
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                                                                   ADDRESSEE:
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                                                                                                                                                        COUNTRY:
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US-08-685-576-1
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APPLICANT: Zhang, Sheng
APPLICANT: Yu, Wan
IIILE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
ITTLE OF INVENTION: GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Pennie & Edmonds
T: 1155 Avenue of the Americas
New York
: New York
561 RPEEKRPKSVTASVLRPSPAPPL 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
                                                                                                                                                                                 Sequence 12, Application US/09442100 Patent No. 6359193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 652
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
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amino acid
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                                                                                                                                                                                                                                                                               APPLICANT: Xu, Tian
APPLICANT: Tao, Wufan
APPLICANT: Wang, Weiyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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Matches 106; Conserv
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537 LYAWLMSTLSRADGSQMAEERIMEEQQKGRSSKKTKKKKKVRPLSREITMSQAYQNMCAG 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                653 KYSPPPQSPELYVAASKHFQQAKMILENIPNPDHEVNRILKVAKPNFVVMKLLAG---GH 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 LIVLIAFTKKETSAVAEAQKLMVQAADLLSAIHNSLHHGIQAQNDTTKGDHPIMMGFEPL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 HÓCDHABIKBALSÍKRBÍAQKVKDEPQQNSGVSTHHRDLFVRÍKCTLTSRGRSINIKSAS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FGTHLMQDMVKDALRSFVDPPVLSPKCYLYNNHQAKDCIDSFVT-HCVRPFCSLI 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 YKVIHITGHLVVNAKGERLLMAIGRPIPHP----SNIEIPLGTSTFLTKH-----SLD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 QIHGHNRARQRDKLGHILEEFATLQDEFMTFYFN-----RAEKVDAALHTMLLKQEPQRQ 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SLAQQTAASEQKEQHHQAAETEKEPEKAADPEIIAQETKETVNTP 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 IHTS-----ELQAKPLQLESEKA--EKTIEETKTIATIPPVTATSTADQIKQLPESN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 MRITIAFLK----IRE----MLÓFVPSLRDCNDDIKQDÍETAEDQQEVKPKLEVGTEDW 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 VN----QRILLPPTFPRYAKIIKREEMVNYFARLIDRIKTVCEVVNLTNLHCILDFFCEFS 359
   ---ELQDER-----DSLAAQLEITLTKADSEQ 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 HLACLG----TWVL----YHNLR----IMIQYLLSGFELELYSMHEYYYIYWYLSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              883 RYRFLGKYGGYCWILSQATIVYDKLKPQSVVCVNYVISNLE----NKHEIY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 IDLRVTGMLKDVEDDMORRVKSTRSROGEERDPEVELEHQOCLAVFSRVKFTRVL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.7%; Score 105.5; DB 4; Length 1507; Best Local Similarity 17.2%; Pred. No. 0.74; Matches 107; Conservative 101; Mismatches 242; Indels 173;
                                                                              553 MAEERIMEEQQKGRSSKKTKKKKKRPL---SREITMSQA 589
                                                                                                                          APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STACED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 375
LENGTH: 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     710 KKESKVPPEFDFSAHKYFPVVKL 732
                                                                                                                                                                                                                                                                       RESULT 14
US-09-914-259-37
; Sequence 37, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophilia melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 EQ-----SPCVLSRSL-
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238 KHNYIHRDIKPDNLLLDRYGHLKLSDFGLCKPLDCSTLEE 277	463 EFWIFYFNRAEKVDAALHTWLLKQEPQRQHLACLGTWVLYHNLRIMIQY 511	278 KDFSVGDNANGGSRSDSPPAPKRTQQEQLEHWQKNRRMLAYSTVGTP 324	STI	325 DYIAPEVLLKKGYGMECDWWSLGAIMYEMLVGYPPFYSDDPMSTCRKIVNWK 376	549 DGSQMAEERIMEEQQKGRSSKKTKKKKKRPLSREITMSQAYQNMCAGM 597	377 NHLKFPEBAKLSPEAKDIISRLLCNVTERLGSNGADEIKVHSWFKGIDWDRIYQMEAA 434	GKVRKPKFFLDSEQVRYEHRFP		FNK	494 VPGMVELKKTNTKPKKFTI 512
23	46	27	512	32	54	37	59	435	651	49
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Search completed: August 10, 2004, 21:52:30 Job time: 23 secs